

10 RESULT 9
 AC R60496 standard; Fluctuon (28) AA.
 ID 860496,
 DT 28 MAR-1995 (first entry)
 DE Linoleic acid desaturase (Lsd)
 KW Linoleic acid desaturase [EC:1.3.1.64]
 KW transgenic plant; crop improvement; yeast artificial chromosome;
 NM YAC; linolenic acid.
 OS Brassica napus.
 UN M0941837-A.
 PD 18-AUG-1994.
 PF 04-FEB-1994; 001321.
 PR 05-FEB-1993; NS-014431
 FR 22-NOV-1993; NS-156551.
 PA (MONS) MONSANTO CO.
 PA (UNMS) UNIV MICHIGAN STATE
 PI Arcade, 27A, Gilbert St, East Lansing, MI, 48824-1315;
 DR HT1; 94-279358-34.
 DR N-PSDB; Q71203.
 PT Genetically transformed plants with altered linoleic acid
 PT content - contg recombinant, double stranded DNA encoding
 PT linoleic acid desaturase, or the antisense of the coding
 sequence
 FT
 FT Cistocaine; Page 67 of 77; 144pp; English.
 CC cDNA encoding the linoleic acid desaturase (Lsd) of R. rapum
 CC isolated from a YAC library and pET 220 and AcclA methods to
 CC process. Isolated DNA was amplified using the primers given in
 CC U7104.09, and used to screen YAC libraries. The first gene was
 CC identified in YAC EM7211.
 CC Sequence 384 AA;

[illegible]

DT 01-OCT-1993 (first entry)
DE Sequence of mitochondrial delta-15 desaturase.
FM Isolated by complementary DNA library screening of rat liver.
GC Glycine Max clone pGFI.
GN M0431245.A.
PO 10-MAY-1993.
PP 04 SEP 1992; 0109784.
PB 04-DEC-1991; 05-804759.
PA (DUPLO) DO POINT DE MEMPHIS & Co E.L.
PI Brown, T., Grant LE, Kinney AJ, Fierman WM, Winterhagen AM,
P1 Yadaav NS?
P2 WPI: 93-197063/24.
P3 N-PSDB: 043207.
PT Isolated nucleic acid fragment, for plant lipid compou.
PT modification: complementary DNA and sequence encoding fatty
PT acid desaturase or related enzyme with high amino acid identity to
PT specific polypeptide
P4 Description: Fragment 144-147, 167bp; English.
P5 Fragment was isolated from a cDNA library using a 5' to Hind III
P6 fragment containing wild-type genomic DNA as a control and
P7 hybridization probe. One of the sequencing primers is 5' to the PCR3
P8 insert was also used. The identity of the expression product of PCR3
P9 as the delta-15 desaturase was confirmed by digestion was verified by
P9 its biological overexpression in plant tissues. Genetized regions of
P9 837/92 are deleted in degraded acid with acid 101 hybridization as
P9 well as a 5' to Hind III fragment from the cDNA. The sequences
P9 of nucleic regions are given as 043123 043224. Nucleotide delta-15
P9 desaturase cDNA was used as a hybridization probe to isolate a
P9 complementary DNA from rat liver. The complementary DNA was
P9 deposited under ATCC 68814.
SQ Sequence: 380 AA;

[illegible]

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CC 060664 as claimed. A method for identifying fatty acid desaturases
 CC encoding fatty acid desaturase and related enzymes is claimed
 CC which comprises: comparing AA to protein to determine if it is a
 CC fatty acid desaturase sequence; identifying conserved sequences of
 CC 4 or more AA's; designing primers for PCR based on the conserved
 CC sequences; and using the primer to amplify sequences encoding fatty
 CC acid desaturases and desaturase related enzymes.

Sequence: 383 AA

Query Match

89.53% Exact: 270/304, OR 10%, Length: 383

Best local similarity: 91.43% Exact: 270/304, OR 10%, Length: 383
 Matches: 351/3, Conservative: 87, Mismatches: 24/3, Indels: 1/3, Gaps: 1/3

Db 1 mdaagmgpspskscetshktrpccpffvga-llh-afph-ctfs-fst-ah-ll-
 QY 1 MGAGGMAVSPPSKSEETDINKVCHHTFTEVLELNKAFPHFNSIFNSFSLMDI 60
 Db 61 llaecfyvatcyfllpmlpsylamplywaagcgvllgwwahocghaalsdyqidd 120
 QY 61 llaecfyvatcyfllpmlpsylamplywaagcgvllgwwahocghaalsdyqidd 120
 Db 121 tvglllshfllvfyfwkysttrthantjelerdewtpr-sq-sqstaststftrv 170
 QY 121 tvglllshfllvfyfwkysttrthantjelerdewtpr-sq-sqstaststftrv 170
 Db 121 tvglllshfllvfyfwkysttrthantjelerdewtpr-sq-sqstaststftrv 180
 QY 121 tvglllshfllvfyfwkysttrthantjelerdewtpr-sq-sqstaststftrv 180
 Db 180 mltvqllpmlplafnvsqfpydrtjphfpapryndrtqlysdagllavayl 239
 QY 180 mltvqllpmlplafnvsqfpydrtjphfpapryndrtqlysdagllavayl 239
 Db 181 mltvqllpmlplafnvsqfpydrtjphfpapryndrtqlysdagllavayl 240
 QY 181 mltvqllpmlplafnvsqfpydrtjphfpapryndrtqlysdagllavayl 240
 Db 241 lgyaaagmasmactygvplllmalvlllyqtrhpslphysosowdrtqjatrdr 299
 QY 241 lgyaaagmasmactygvplllmalvlllyqtrhpslphysosowdrtqjatrdr 299
 Db 241 lgyaaagmasmactygvplllmalvlllyqtrhpslphysosowdrtqjatrdr 300
 QY 241 lgyaaagmasmactygvplllmalvlllyqtrhpslphysosowdrtqjatrdr 300
 Db 300 dygllnkvthnldthvahlstfmpynameakalkpdlgdyatdrtpyvanyrea 359
 QY 300 dygllnkvthnldthvahlstfmpynameakalkpdlgdyatdrtpyvanyrea 359
 Db 301 dygllnkvthnldthvahlstfmpynameakalkpdlgdyatdrtpyvanyrea 360
 QY 301 dygllnkvthnldthvahlstfmpynameakalkpdlgdyatdrtpyvanyrea 360
 Db 360 keciyepdrtqekkytwynkl 383
 QY 360 keciyepdrtqekkytwynkl 383
 Db 361 keciyepdrtqekkytwynkl 384
 QY 361 keciyepdrtqekkytwynkl 384

RESULT 2

ID R53697 standard; Protein; 383 AA.

AC R53697

DT 09-NOV-1994 (first entry)

DE Sequence of microsomal delta-12 desaturase.

KM Fatty acid desaturase; lipid; unsaturated; transgenic plant.

OS Arabidopsis thaliana.

PN W69411516 A.

PD 26 MAY 1994.

PE 15-OCT-1993; 009961.

PR 17-NOV-1992; 05 97333.

PA (DDP)) DU PONT DE NEMOURS & CO E. I.

PI Lightner JE, Okuley JJ

DR WPI 94-183519/22.

DR N-PSDB; 066068.

PT Genes for fatty acid desaturase enzymes patent application of

PT Plant lipid composition.

PC Claim 13; Page 112 137 147pp; English.

CC The gene sequence to 060664 was isolated by screening Arabidopsis

CC genomic DNA library using radiolabeled cDNA insert, performing

CC positively-hybridizing plaques, and subcloning a 6kb Hind III insert

CC fragment from the phage DNA in phoscript vector. Comparison of the

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CC sequence of the gene (060664) and the cDNA (060664) revealed the
 CC presence of a single insertion of 1134 bp at a position between
 CC nucleotides 88 and 89 of the cDNA, which was a 100% identity
 CC insertion in the cDNA. A method for identifying fatty acid desaturases
 CC encoding fatty acid desaturases and related enzymes is claimed
 CC which comprises: comparing the sequences of protein to 4 or more
 CC fatty acid desaturase 1 type fatty acid desaturase conserved
 CC sequences of 4 or more AA's; designing primers for PCR based on
 CC the conserved sequences; and using the primer to amplify sequences
 CC encoding fatty acid desaturases and desaturase related enzymes.

Sequence: 383 AA

Query Match

89.53% Exact: 270/304, OR 10%, Length: 383

Best local similarity: 91.43% Exact: 270/304, OR 10%, Length: 383
 Matches: 340/3, Conservative: 23/3, Mismatches: 20/3, Indels: 1/3, Gaps: 1/3

Db 1 mdaagmgpspskscetshktrpccpffvga-llh-afph-ctfs-fst-ah-ll-
 QY 1 MGAGGMAVSPPSKSEETDINKVCHHTFTEVLELNKAFPHFNSIFNSFSLMDI 60
 Db 61 llaecfyvatcyfllpmlpsylamplywaagcgvllgwwahocghaalsdyqidd 120
 QY 61 llaecfyvatcyfllpmlpsylamplywaagcgvllgwwahocghaalsdyqidd 120
 Db 121 tvglllshfllvfyfwkysttrthantjelerdewtpr-sq-sqstaststftrv 170
 QY 121 tvglllshfllvfyfwkysttrthantjelerdewtpr-sq-sqstaststftrv 170
 Db 121 tvglllshfllvfyfwkysttrthantjelerdewtpr-sq-sqstaststftrv 180
 QY 121 tvglllshfllvfyfwkysttrthantjelerdewtpr-sq-sqstaststftrv 180
 Db 180 mltvqllpmlplafnvsqfpydrtjphfpapryndrtqlysdagllavayl 239
 QY 180 mltvqllpmlplafnvsqfpydrtjphfpapryndrtqlysdagllavayl 239
 Db 181 mltvqllpmlplafnvsqfpydrtjphfpapryndrtqlysdagllavayl 240
 QY 181 mltvqllpmlplafnvsqfpydrtjphfpapryndrtqlysdagllavayl 240
 Db 240 yryaaagmasmactygvplllmalvlllyqtrhpslphysosowdrtqjatrdr 299
 QY 240 yryaaagmasmactygvplllmalvlllyqtrhpslphysosowdrtqjatrdr 299
 Db 241 lgyaaagmasmactygvplllmalvlllyqtrhpslphysosowdrtqjatrdr 300
 QY 241 lgyaaagmasmactygvplllmalvlllyqtrhpslphysosowdrtqjatrdr 300
 Db 300 dygllnkvthnldthvahlstfmpynameakalkpdlgdyatdrtpyvanyrea 359
 QY 300 dygllnkvthnldthvahlstfmpynameakalkpdlgdyatdrtpyvanyrea 359
 Db 301 dygllnkvthnldthvahlstfmpynameakalkpdlgdyatdrtpyvanyrea 360
 QY 301 dygllnkvthnldthvahlstfmpynameakalkpdlgdyatdrtpyvanyrea 360
 Db 360 keciyepdrtqekkytwynkl 383
 QY 360 keciyepdrtqekkytwynkl 383
 Db 361 keciyepdrtqekkytwynkl 384
 QY 361 keciyepdrtqekkytwynkl 384

RESULT 3

ID R95579 standard; Protein; 384 AA.

AC R95579

DT 10-SEP-1996 (first entry)

DE Rappa fatty acid hydroxylase-lesquerelle acid; transgenic plant;

KM Rappa fatty acid hydroxylase; Lesquerella alba; transgenic plant;

KM Rappa fatty acid hydroxylase; Lesquerella alba; transgenic plant;

KM Rappa fatty acid hydroxylase; Lesquerella alba; transgenic plant;

OS Lesquerella tendleri.

PN W69410075 A1.

PD 04 APR 1996.

PE 25 SEP 1995; 011855.

PR 26 SEP 1994; US 314506.

PP 11 OCT 1994; US 320082.

PE 20 SEP 1995; US 320082.

PA (BPO)) BRIDG P.

PA (CONE)) SOMERVILLE C.

PA (VINO)) VAN DE LIND P J.

Pd	Z6-MAY-1994.
Pf	15-OCT-1993; 009987.
Pf	17-NOV-1992; US-97339.
Pa	(DUPC) DU PONT DE NEMOURS & CO E. I.
P1	Lighthouse JE, Okuley JJ;
DR	WP17 94-183515/22.
DR	N-FEDB; G66071.
PT	Genes for fatty acid desaturase enzymes - permit alteration of plant lipid composition.
FT	Plant lipid composition.
P5	Ciam 13; Page 124, 126; 147pp English.
CC	Corn microsomal delta-12 desaturase cDNA was isolated using a PCR approach. A cDNA library was made to allow a MPRA from developing corn embryos. This library was used as template for PCR using sets of degenerate oligos 503 (G66071) and 635A/B (G66073), G66079) as sense and antisense primers. Respectively, NCS and RPA/RAP controls to stretches of Abbs 161-164 and 316-326, respectively, of 853497, which are conserved in most microsomal delta-12 desaturases. A PCR product of 720bp was purified and used as a probe for screening the cown cDNA library. A plaque was pulled and found to encode microsomal delta-12 desaturase truncated at the 3' end. This cDNA was used to probe the corn cDNA library again. The clone coding the longest insert, designated Pfad-1 was sequenced completely. (G66071). An isolated nucleic acid fragment wherein the nucleic acid identity is 90% or greater to G66071 as claimed. A method for isolating nucleic acid fragments encoding fatty acid desaturases and related enzymes is claimed. CC which comprises: separating AA sequences on HPLC; HPLC and other fatty acid desaturase sequences; identifying selected sequences; CC 4 or more AAs; designed degenerate oligos based on the conserved sequences; and using the oligos to isolate sequences encoding fatty acid desaturases and desaturase related enzymes.
CC	Sequence 367 AA;
Query Match	66.4%; Score 3607; of 109; Length 367;
Best local Similarity	68.6%; Ident. No. 1,400-184;
Mismatches	264; Conservative 49; Mismatches 68; Indels % Gap 3;
Dd	7 mtekerkqeqaratgtaamqpvspevrrptlgrdkkaprotetevskisyvhd 66
Gy	1 MASGRWVGSEIPEKPKLILHLEFETPTSTITNPGLESAIPGEFEESTPTSPSHIMRT 60
Dd	67 vlsaalilyfalaliprlpsrlylamelylagggvotgwvtahocghafsyveln 126
Gy	61 IIASCEFYATATTEFLIRHLISLAWMAQGVLLDSVAIAHEHCINHAENSYGMND 120
Dd	127 vsqvlstsslmwryfwskylshihentjksloedovfrkkleilpwv ryuyrmprvg 186
Gy	121 TVALTRPCFLVFECMWYCHDHCDHDLGLALAEVEEIEKSDIFWDEGE ENKLSRET 179
Dd	187 whlvagtlawpyllacnasgyeyer lachlfyfyndreagifysdagvyavayg 245
Gy	186 WLVTVUUTLAWMLHLANVSAGETLOOKKCHAFERATYNSRRLKLYLSDAATLAAGCG 239
Dd	245 lyklaaafwywvvuvuwvlylwvkwlytylqtffpslphrydsowwdwlgallad 305
Gy	240 LFRFAAAAGVAMAVMTTGVYLAWYFNNTTLIDKGTGSLURDTSCFMHWPRALATYE 299
Dd	306 rldgvalrvfnhlctdvahhlstmplyhamcatkaaplilsgyhbfprpvakatew 365
Gy	300 RNYGLIKRKFNRIIDTGVAHNHRSCMNPYMKAATAKAPLTLDLYVOGDERRUYNAAMGP 259
Dd	366 aqecluvepe--dtkyflwvdkl 387
Gy	360 ASCLTYVEDRPQEKSKYVTWNKKL 364

ID	RESULT	6
1D	R53702 standard; Proteolip, 387 AA.	
AC	R53702?	
PT	09-MAY-1994 (first entry)	
DE	Sequence of cDNA from <i>Helicoverpa zea</i> delta 12 desaturase deduced from the cDNA	
DE	in plasmid pRFL97C-42.	
FM	Fatty acid desaturase, lipid unsaturated, transgenic plant.	
OS	<i>Helicoverpa zea</i> .	
PN	W09411516.A.	
PP	26-MAY-1994.	
PF	15-OCT-1993; 0099871.	
FE	17-MAY-1992; 05-971339.	
PA	(DIPPO) ON POINT DE MEMOIRS 6 CO E. I.	
P1	14-APR-90; 0040503?	
DR	W01719418315/22.	
DR	N (PDB); 046073.	
PT	Genes for fatty acid desaturase enzymes - permit alteration of	
PT	plant lipid composition	
PC	Claim 13; Page 121, 133; 147pp; English.	
CC	A-omega fatty acid desaturase from <i>Helicoverpa zea</i> deduced from sequencing	
CC	data from (S) type IV, (20-25 DAP) was sequenced. Partially labeled	
CC	with 10-12-13-14-15-16-17-18-19-20-21-22-23-24-25-26-27-28-29-30-31-32-33-34-35-36-37-38-39-40-41-42-43-44-45-46-47-48-49-50-51-52-53-54-55-56-57-58-59-60-61-62-63-64-65-66-67-68-69-70-71-72-73-74-75-76-77-78-79-80-81-82-83-84-85-86-87-88-89-90-91-92-93-94-95-96-97-98-99-100-101-102-103-104-105-106-107-108-109-110-111-112-113-114-115-116-117-118-119-120-121-122-123-124-125-126-127-128-129-130-131-132-133-134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-8	

[illegible][illegible]

Eb	364	IYGEWIAIIVMLdIvYlhhgghdeIpywceKmsyIsgitIdIdydlImnhdI	365
Gy	285	FVVEELITNPLSLTINLNGHTRDDEEDIDGDMDFRGLATVDRDQIGGGTETRT	312
Dc	364	-gttwhblfpqahphylwaetckkvrt	396
Gy	313	TDTVAHPFSTMGHMAALRALNNILRETYG	346

RESULT 15

10 R60499 standard; Protein; 446 AA

AC R60499;

07 28-MAR-1995 (first entry)

DE linoleic-acid-desaturase fad₉.

KM linoleic-acid-desaturase, fad₉; transgenic plant; crop improvement

KW linolenic acid.

OS Arabidopsis.

PN M09418337-A.

ED 18-AUG-1994.

FF 04-FEB-1994; U01321.

PR 05-FEB-1993; U5-014431.

PR 22-NOV-1993; U5-156551.

PA (MONS) MONSANTO CO.

FA (UNMS) UNIV MICHIGAN STATE.

PI Arcodel VDA, Gibson SL, Kishore OM, Ruff TG, Somerville CR;

DR WPI; 94-279758/74.

DR N-PSDB; Q71210.

PM Genetically transformed plants with altered linolenic acid

PT content - conif recombinant, double stranded DNA encoding

PT linolenic acid desaturase, or the antisense of the coding

PT sequence

PS Disclosure; Page 75-77; 144pp; English.

CC The cDNA sequence and deduced amino acid sequence of linoleic-

CC acid-desaturase fad₉ of Arabidopsis are provided

Sequence 446 AA;

50

Query Match	22.1%;	Score 667;	DB 11;	Length 446;
Best Local Similarity	37.4%;	Fred. No. 1.25e-5;		
Matches	106;	Conservation 110;	Indels 29;	Caps 14;

[illegible]

Submitted: 12 March 29 1997
 Accepted: 27 Dec 97

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2

12	705	23.3	380	7	E37595	Sequence of <i>Myoblastoma</i>	3,406-54
13	706	23.3	404	7	R34594	Sequence of plasmid	2,773-54
14	703	23.2	446	7	R37593	Sequence of plasmid	5,276-54
15	703	23.2	446	11	R60499	Imidic acid desatur	5,276-54
16	481	22.5	425	11	R65956	Imidic acid desatur	6,446-52
17	289	9.5	156	7	R37598	Sequence of a plasmid	2,908-16
18	259	7.5	418	11	R46501	Imidic acid desatur	7,746-11
19	127	4.2	176	7	R37597	Sequence of a plasmid	1,166-01
20	113	3.7	354	7	R24152	Imidic acid desatur	1,316-09
21	113	3.7	354	17	R98456	Synthetic <i>Myoblastoma</i>	1,316-09
22	100	3.3	2516	14	W01884	Neuronal intermediate	1,146-01
23	100	3.3	2516	14	W01884	Neuronal intermediate	1,146-01
24	98	2.2	289	7	R27264	Imidic acid desatur	1,586-01
25	93	3.1	481	4	R00066	Imidic acid desatur	3,506-01
26	93	3.1	481	4	R00066	Imidic acid desatur	3,506-01
27	93	3.1	481	4	R00066	Imidic acid desatur	3,506-01
28	91	3.0	219	4	R40816	Imidic acid desatur	4,806-01
29	91	3.0	219	4	R40816	Imidic acid desatur	4,806-01
30	90	3.0	380	5	R20038	Imidic acid desatur	5,416-01
31	97	3.8	404	7	R41151	Imidic acid desatur	5,416-01
32	90	3.0	471	12	R47492	Imidic acid desatur	5,416-01
33	90	3.0	471	12	R47492	Imidic acid desatur	5,416-01
34	90	3.0	471	12	R47492	Imidic acid desatur	5,416-01
35	90	3.0	471	12	R47492	Imidic acid desatur	5,416-01
36	90	3.0	471	12	R47492	Imidic acid desatur	5,416-01
37	87	2.9	381	4	R40806	Imidic acid desatur	5,416-01
38	87	2.9	381	4	R40806	Imidic acid desatur	5,416-01
39	86	2.9	619	5	R27651	Imidic acid desatur	7,656-01
40	84	2.4	674	16	R46508	Imidic acid desatur	7,656-01
41	84	2.4	674	16	R46508	Imidic acid desatur	7,656-01
42	86	2.9	2161	6	R33535	Imidic acid desatur	7,656-01
43	84	2.4	2161	14	R71002	Imidic acid desatur	7,656-01
44	88	2.9	2161	14	R71002	Imidic acid desatur	7,656-01
45	87	2.9	2161	14	R71002	Imidic acid desatur	7,656-01

ALIGNMENTS

RESULT 1

10. R53998 Standard, Protein;
A⁺ R53698;

09-NOV-1994 (first entry)

U.S. (FZ1634,
Party 2014, 2015)

BRASSICA napoli.
PIN W09411516-A.

FD 26-MAY-1994.
 PF 15-OCT-1993; 11:2487.

PH 17-NOV-1992; US-971339,
IPA (DIPD) IN PORT OF NEMOURS

PI: Lightner OE, Okuley JJ;
WPI: 94-183515/22.
DK

60990

Plant and composition

with library made with poi

with 133, a sealed portfolio of photographs 1450, designated portfolio

1. $\text{H}^1(\mathbb{R}^n, \mathbb{R}) \cong \mathbb{R}^n$

3

CC 066164 is claimed: A method for isolating nucleic acid fragments
 CC encoding fatty acid desaturases and related enzymes is claimed
 CC which comprises: comparing AA sequences in F3647, F63702 and other
 CC fatty acid desaturase sequences, identifying conserved sequences of
 CC 4 or more AAs; designing degenerate oligos based on the conserved
 CC sequences; and using the oligos to isolate sequences encoding fatty
 CC acid desaturases and desaturase related enzymes.

54 Sequence 383 AA;

Query Match 99.7% Score 2747, DB 10, Length 383;
 Best local Similarity 99.7% Pos. 1, 466-254;
 Matches 346; Conservative 7; Mismatches 29; Indels 1; Gaps 1;

Db 1 maaqgmprssksseldtkkrpekrpsvqdkkafprckkpsrfsylsdi 60
 ||||||| : ||||||| ||||| : ||||||| ||||||| ||||||| |||||
 QY 1 MAAQGMQVSPSKSSKSELTNNKVPETTPETV-3LKA1FPPKPPSPSYLMDI 60
 Db 61 niasctyyaatytpilppplsytafwlywaagqcytawlyadecphasdyqdd 120
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 61 NIASCTYYAATYTPILPPPLSYTAFWLYWAGQCYTAWLYADECPHASDYQDD 120
 Db 121 twglthslfllyovfswkyshtrhnsstlerdevfpr-sqtssylastlftiv 174
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 121 TWGLTHSLFLLYOVFSWKYSHTRHNSSTLERDEVFPR-SQTSYLASTLFTIV 174
 Db 180 mlwqtlwplylaflavsrpydgtachlfnapiyndeqlqylsdagllawcy 234
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 181 MLWQTLWPLYLAFVLSRPRYDGTACHLFPNAPIYNDQLQYLSDAGLLAWCY 234
 Db 240 lyyaagvysacchllfrrllscgyllylqthpslphydseswkllyalavd 294
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 241 YRYAAGVYSAWCFYCVPLLVNGLFLVLTLLGHTPSLPHSSMDLRLQALATVR 300
 Db 300 dyglngkthnltthvabhlstmpnyameakkaikpilyqfagprvkwkmyea 319
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 301 DYGLNGKVNHTDTHVAHNLFTMFRHMAFKAIRKPLDSELYQLHGPVVAAMRKA 360
 Db 360 keciyepdrgdkkyywmynk 383
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 361 KECIYEPDREGKGVFWYNNKL 384

RESULT 2

ID R03697 standard; Protein 383 AA.
 AC R03697;
 DT 09 NOV 1994 (first entry)
 DE Sequence of microsomal delta-12 desaturase.
 KW Fatty acid, desaturase; lipid, unsaturated, transgenic plant.
 OS Arabidopsis thaliana.
 FN M0941316-A.
 PD 26 MAY 1994.
 PE 15-OCT-1994; 009961.
 PR 17 NOV 1992; US 977339.
 RA (DUEV) DU POINT DE NEMOURS & CO E. I.
 RI Lighter JE, Okuley JJ;
 DR WP1; 94-183519/22.
 DR N-PSDB; 066068.
 PT Genes for fatty acid desaturase enzymes permit alteration of
 PT plant lipid composition.
 PS Claim 13; Page 112-114; 147pp. English.
 CC The gene cDNA for *Δ6* desaturase was isolated by screening Arabidopsis
 CC genomic DNA library using radiolabeled PCR2b cDNA insert, purifying
 CC positively hybridizing plaques, and subcloning a 6kb Hind III insert
 CC fragment from the phage DNA in plasmid vector. Description of the

CC sequences of the gene (066163) and the cDNA (066162) revealed the
 CC presence of a single insertion of 1174 bp at a point between
 CC nucleotides 88 and 89 of the cDNA, which is a nucleotide 5' to the
 CC initiation codon. A method for isolating nucleic acid fragments
 CC encoding fatty acid desaturases and related enzymes is claimed
 CC which comprises: comparing the sequences of F63702 and other
 CC fatty acid desaturase fatty acid sequences; identifying conserved
 CC sequences of 4 or more AAs; designing degenerate oligos based on
 CC the conserved sequences; and using the degenerate oligos to isolate
 CC sequences encoding fatty acid desaturases and desaturase related
 CC enzymes.

59 Sequence 383 AA;

Query Match 90.6% Score 2742, DB 10, Length 383;
 Best local Similarity 89.6% Pos. 1, 106-253;
 Matches 344; Conservative 21; Mismatches 18; Indels 1; Gaps 1;

Db 1 maaqgmprssksseldtkkrpekrpsvqdkkafprckkpsrfsylsdi 60
 ||||||| : ||||||| ||||| : ||||||| ||||||| ||||||| |||||
 QY 1 MAAQGMQVSPSKSSKSELTNNKVPETTPETV-3LKA1FPPKPPSPSYLMDI 60
 Db 61 niasctyyaatytpilppplsytafwlywaagqcytawlyadecphasdyqdd 120
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 61 NIASCTYYAATYTPILPPPLSYTAFWLYWAGQCYTAWLYADECPHASDYQDD 120
 Db 121 twglthslfllyovfswkyshtrhnsstlerdevfpr-sqtssylastlftiv 174
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 121 TWGLTHSLFLLYOVFSWKYSHTRHNSSTLERDEVFPR-SQTSYLASTLFTIV 174
 Db 180 mlwqtlwplylaflavsrpydgtachlfnapiyndeqlqylsdagllawcy 234
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 181 MLWQTLWPLYLAFVLSRPRYDGTACHLFPNAPIYNDQLQYLSDAGLLAWCY 234
 Db 240 lyyaagvysacchllfrrllscgyllylqthpslphydseswkllyalavd 294
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 241 YRYAAGVYSAWCFYCVPLLVNGLFLVLTLLGHTPSLPHSSMDLRLQALATVR 300
 Db 300 dyglngkthnltthvabhlstmpnyameakkaikpilyqfagprvkwkmyea 319
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 301 DYGLNGKVNHTDTHVAHNLFTMFRHMAFKAIRKPLDSELYQLHGPVVAAMRKA 360
 Db 360 keciyepdrgdkkyywmynk 383
 ||||||| : ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 QY 361 KECIYEPDREGKGVFWYNNKL 384

RESULT 3

ID R03697 standard; Protein 384 AA.
 AC R03697;
 DT 10-SEP-1996 (first entry)
 DE Kappa fatty acid hydroxylase, Δ^12 -desaturase.
 KW Kappa fatty acid hydroxylase, desaturase; fatty acid, transgenic plant;
 RA oilseed; seed oil; rapeseed; canola; Brassica juncea; variety, flax;
 RA sunflower; safflower; cotton; capasa; soybean; peanut; coconut;
 RA oil palm; corn.
 FN Lesquerella tendleri.
 PD 04-APR-1996.
 PT 25 SEP-1995; 011852.
 PR 26-SEP-1994; US-314596.
 PR 11 OCT-1994; US 320982.
 PR 20-SEP-1995; US 320982.
 PA (BR001) BROOK T.
 PA (G0MF) SOMERVILLE C.
 PA (V000) VAN DE UNO F. J.

247 TMDVAGTILANVEHNTTVAHNFSTMEHNAMEATPAHPIIGSYQI HCTVDVNAW 316
 350 KTEKCECTIIVPGDAPTGTATWYRK 386
 357 WEEMAEILVDEHGDGELNVAWNA 392
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Search completed: Wed Dec 17 17:22:15 1997
Job time : 1105 secs.

066669 fatty acid desaturase and related enzymes is claimed.
CC encoding fatty acid desaturase and related enzymes is claimed.
CC which comprises: comparing AA sequences in a first part; and
CC fatty acid desaturase sequence; identifying conserved sequences of
4 or more AAs; designing oligonucleotides based on the conserved
CC sequences; and using the oligonucleotides and sequences encoding fatty
CC acid desaturases and desaturase related enzymes.
Sequence 383 Aa.

Query Match	90.26%	239.44%	16.10%	100.00.00%
Best Local Similarity	92.48%	247.35%	1.200.00%	
Matches	3557	Conservative	77	Mismatches 217
				Indels 17
				Gaps 17

```

Db 1 mjaagimqpspskkskshdmlhvpeslptvghlkaagpshktsipstshwdf 60
QY 1 MAAAGAGVCSFPEKELNNKAEVPELLEHIVQELLLAHHFQFPSPFSESYLMDI 60
Db 61 hiascflyvallyfpllpmlplyfawpilyacqgcvtlygwiaheeqhaafcdqwd 120
QY 61 hAAQCYVATYFPELLEHLELYAWPILYAWPQGVLYGVAIVANQCHSAFSDYWD 120
Db 121 tvgllthsllyvpyfawkyshn rhshnsglerdevtpr-sqtsqtsastltgtv 179
QY 121 TPGCTHCELTATFQCRKSHHCEHMMHMLLALANLSTYTHKCEIHWQVYLNPLRGTV 180
Db 180 mlvtgflawpilyafafsvsrydsqglchfipkaplyndertqlvysdaqllavcy 239
QY 181 MLTQFTLQWPLYAFVNSGSEYDQGFALHHEHNAFTHNREHLYVSDGGLAVATRL 240
Db 240 lrpjagaygrasncvclpplllnngsflytygqthprsplydsscwkwlratalvcd 299
QY 241 PFIAAVQVAAASWVFTYVPLLVNCELVLLTHLPSLHPSLSTAFSEFWMLKAAATVTR 300
Db 300 dygllngflhualdtheahhlscmplyhamatkauplllyvqfgrfpvukamkroa 359
QY 301 DYGLLNRYVNNLTCTGYVAMHHSNMLSTYNNMAATATATFEDCTQLHQRVYVAAWMBFA 360
Db 360 kaclywepdrqpekkyvlywnk 383
QY 361 KECITYEDRQGEKQCVFVNNKL 384

```

RESULT 2
 ID R53697 standard; Protein; 363 AA.
 AC R53697;
 DT 09-NOV-1994 (first entry)
 DE Sequence of mitochondrial 3'-15.19 kb-ntase.
 FM Fatty acid; decarboxase; lipid; unsaturated; transgenic plant.
 KM Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 FN M0941516-A.
 PD 26-MAY-1994.
 PR 15-OCT-1993; 009687.
 PR 17-NOV-1992; 08-077319.
 PA (DDBP) DDBPONT DE NEMO3000 & CO L.
 PI Lightner JE. Okuley JJ;
 DH WPJ; 94-183515/22.
 DH N-F5DB; 066068.
 FT Genes for fatty acid synthase enzyme protein cleavage of
 PT plant lipid composition
 PS Claim 13; Page 112-114; 147PP; English.
 CC The gene sequence of 3'-15.19 kb was obtained by screening A. thaliana
 CC genomic DNA library using radiolabeled pGE2b cDNA insert, purifying
 CC positively-hybridising plasmid, and subcloning a 6kb Hind III insert
 CC fragment from the plasmid DNA in phage lambda vector. Comparison of the

[illegible]

Query Match 90.3%; Score 2735; DR 16; Length 383;
Best Local Similarity 89.3%; Pred. No. 3, 748 253;
Matches 343; Conservative 21; Mismatches 19; Indels 1; Gaps 1;

[illegible]

RESULT	3
ID	p95679 standard; Protein; 384 AA.
AC	R95679;
RT	10-SEP-1996 (first entry)
DE	Kappa fatty acid hydroxylase, plant.
KW	Kappa fatty acid hydroxylase; laquerella acid; transgenic plant; cristalloid; seed oil; seed oil; seed oil; Brossesca juncea; amino; 110g crystalline; salmon; codfish; yellow; yellow; fat; coconut; oil; fatty; corn.
CM	laquerella fendleri.
OS	laquerella fendleri.
PN	M09610075-AI.
PD	04-APR-1996.
PE	75-SEP-1995; 011855.
PR	76-SEP-1994; US-514196. 11 OCT-1994; US-520082.
PP	76-SEP-1995; nt 720022.
RA	(HMOU?) BROUIN P.
PA	(SOME?) SOMEVILLE C
RA	(VIAOU?) VAN DUTTOO F J.

ID	Result	% Identity	Accession	Length	Score	Expect	Method
10	NC_044646	Standard, 111,000 bp	363 AA				
AC	Ref0499						
DT	28-MAR-1995 (first entry)						
DE	Linoleic acid desaturase (ad3).						
KM	Linoleic acid desaturase (ad3), oilseed rape; rapeseed;						
KM	transgenic plant; crop improvement; yeast artificial chromosome;						
KM	YAC; linoleic acid.						
OS	Brassica napus.						
PN	W09418331-A.						
PD	16-MAY-1994.						
PF	04-FEB-1994; 001321.						
PR	05-FEB-1993; GS-014431.						
FR	22-NOV-1993; GS-154551.						
PA	(MOMMS) MORGANTO CO.						
PA	(MOMMS) UNIV MICHIGAN STATE.						
PI	Alonzo J.A. Gibson SJ, Kishore SM, Bull TG, Somerville CR;						
DR	WPI; 94-279758/34.						
DR	N-PSNR; Q71293.						
PT	Genetically transformed plants with altered linoleic acid						
PT	content - contig recombinant, double-stranded DNA encoding						
PT	linoleic acid desaturase; in the presence of the polyl						
PT	sequence						
FC	Disclosure; Page 69 70, 100pp; English.						
CC	cDNA encoding the linoleic acid desaturase (ad3) of B. napus was						
CC	associated with a YAC library using pET1-229 and GAD6A markers as						
CC	probes. Isolated cDNA was deposited with the EMBL gene bank in						
CC	Q71204-09, and used to screen YAC libraries. The ad3 gene was						
CC	identified in YAC EM7511.						
CC	Sequence 363 AA;						
DB	Query Match	25.4%	Query 776	1819	Length 3829		
DB	Best Local Similarity 49.8%		From NCBI	167.6%			
DB	Matches 1337	Conservative 49	Maximizes 100	Indels 259	Id+ 144		
DB	AC	NC_044646	Standard, 111,000 bp	363 AA			
DB	QY	21	111	1111	1111	1111	1111
DB	78	1111	1111	1111	1111	1111	1111
DB	85	1111	1111	1111	1111	1111	1111
DB	138	1111	1111	1111	1111	1111	1111
DB	145	1111	1111	1111	1111	1111	1111
DB	191	1111	1111	1111	1111	1111	1111
DB	204	1111	1111	1111	1111	1111	1111
DB	247	1111	1111	1111	1111	1111	1111
DB	263	1111	1111	1111	1111	1111	1111
DB	306	1111	1111	1111	1111	1111	1111
DB	321	1111	1111	1111	1111	1111	1111
DB	346	1111	1111	1111	1111	1111	1111
DB	363	1111	1111	1111	1111	1111	1111
DB	382	1111	1111	1111	1111	1111	1111
DB	400	1111	1111	1111	1111	1111	1111
DB	418	1111	1111	1111	1111	1111	1111
DB	436	1111	1111	1111	1111	1111	1111
DB	454	1111	1111	1111	1111	1111	1111
DB	472	1111	1111	1111	1111	1111	1111
DB	490	1111	1111	1111	1111	1111	1111
DB	508	1111	1111	1111	1111	1111	1111
DB	526	1111	1111	1111	1111	1111	1111
DB	544	1111	1111	1111	1111		

[illegible]

[illegible]

RESULT 15

ID P63499; standard; Protein; 446 AA.
 AC R63499;
 DT 28-MAR-1995 (first entry)
 DE inosinate-acid-3-epimerase [adp]
 DE inosinate-acid-desaturase, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 8

Query Match

23.08; Score 447; MR 11; Length 446;

Best local similarity 38.18; Pred. No. 1.650-533;

Matches 127; conservative 76; mismatches 110; indels 20; gaps 16;

81 eednkqrldpgappfnladraipkhcwkripwkslsyvrdvaiv--falaagay-137

17 ETDNIKHV-PEETPPETVGELESAIDPHICKKOSIINGHSYLIWDIIIASCFYVATYEP 75

Db 138-1-n--nwivplywlaqf.mfwalvighdcqhfnsndpkinsvghl1hsslvpyh 19;

76 LIPPLSYFAWPIYWACQGVLTGVVIAHKUGHAFSDYQWLDVTGGLFHSPLVPRF 135

134 qwrishrbthqnhqhvenjswbrom -se kiynt-ldkp-trffrttjplvm-la-y-p 245

135 *Environmental Protection Agency, "WVAPY and RPPV: A New VOTI GPPLYA 1995*

[illegible]

196 ENVSCEVIGTEAHEHNEITNURHILYISDAITAVCTIYBYAAVOWASMECE 254

[illegible][illegible][illegible]

314 DTHVAHHLESTMPHYHAMEATKAIMP I LÖET YÖ 346

Search completed: Wed Dec 17 11:14:47 1997
Job time: 108 secs.

/home/fuller/dec97/US-08-572-027A-1.rge

23

Query Match	2.9%;	Score 34;	DB 61;	Length 1622;
Best Local Similarity	64.2%;	Prod. No. 1.55e-07;		
Methods	77;	Conserved 40;	Winged 41;	Index 0;
				Caps 9;

[illegible]

Search completed: Wed Dec 17 14:19:05 1997
Job time : 1659 secs.

Release 2.00 John F. Collins, Reconnecting Research Unit,
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MSearch on: n.a. database search, using GML, W. H. Green 1997
Run on: Wed Nov 17 14:59:37 1997, Mosaic time 967.70 seconds

Tabulari caput inl. p. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840. 841. 842. 843. 844. 84

Accession:	U0928572.2 (J)
Description:	(1-115) f.t.m U0928572.f.t.m.ssq
Perfect Score:	1154
N.A. Sequence:	1 ATGCTTATAGTTAAAT.....GGTAAGAATAAATTTC TACCAAGCAGACTTAA.....CATGCTTATTAAT
(Comp:	

Scoring table: TABLE default

[illegible]

Listing first 45 entries

Database:

Database:

Database:

Database:

Statistics: Mean 11.058; Variance 4.501; scale 2.457

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	EB	ID	Description	Pred. No.
1	952	87.5	1381	60	RL0456AT	B. juncus mRNA for cdc	8,304-10
2	811	79.3	1232	59	AF0101AA	Arabidopsis thaliana	0,000-00
3	477	41.3	1554	47	U00000A	Cyanothece sp. 8421-1 m	0,000-00
4	431	33.3	1472	61	CC01501B	C. thermophilus mRNA for	0,000-00
5	352	28.5	1452	67	CC00604D	Glycine max FMY-1 m	0,000-00
6	335	28.2	1440	64	PI029238	Ribonuclease A105	1,470-294
7	121	10.3	1130	42	U00111A	L. pneumoniarum mRNA for	4,584-86
8	56	4.4	1515	61	D43688	Wheat mRNA for pscst	7,450-25
9	39	3.4	1365	68	TO0020A3	Tobacco leaf mRNA for	2,450-11
10	37	3.2	215	17	U28278	Sequence 5, 11m, pten	8,570-10
11	37	3.2	1208	12	U07411	Rice mRNA for W-5, fat	8,570-10
12	37	3.2	1208	12	U07411	Rice mRNA for W-3, fat	8,570-10
13	33	2.9	1383	60	BNA1INDS	Rattus norvegicus thymus	8,570-07
14	34	2.9	1556	64	PC015745	Petroselinum crispum	1,540-07
15	34	2.9	1622	63	SC027617	Sesuvium indicum omega	1,540-07
16	31	2.7	1350	60	AT006A3A	Rattus norvegicus omega	2,280-05
17	30	2.6	1386	60	AT006A3A	Arabidopsis thaliana	1,150-04
18	30	2.6	1409	62	AT006A3A	Arabidopsis thaliana	1,150-04
19	29	2.5	1628	60	AT006A3A	Arabidopsis thaliana	6,610-04
20	29	2.5	1621	59	AT006A3A	Arabidopsis thaliana	6,610-03
21	28	2.4	1413	60	U00000A	Saccharomyces cerevisiae	2,610-03
22	28	2.4	1413	60	BNA000AD	Rattus norvegicus cdc	2,610-03
23	28	2.4	1413	60	AT006A3A	Arabidopsis thaliana	2,610-03
24	28	2.4	1404	59	AT006A3A	Arabidopsis thaliana	2,610-03
25	28	2.4	1404	59	AT006A3A	Arabidopsis thaliana	2,610-03
26	28	2.4	1404	59	AT006A3A	Arabidopsis thaliana	2,610-03
27	25	2.3	106	46	U14747	Saccharomyces cerevisiae	1,250-02
28	24	2.3	1432	60	U00000A	Vigna radiata cdc	1,250-02
29	24	2.3	1432	60	U00000A	Vigna radiata cdc	1,250-02
30	24	2.3	1432	60	U00000A	Vigna radiata cdc	1,250-02
31	23	2.3	1581	63	CC02702A3A	Cyanothece sp. 8421-1 m	1,250-02
32	23	2.3	2936	59	AT006A3A	Arabidopsis thaliana	5,480-02
33	23	2.3	1413	60	U00000A	Saccharomyces cerevisiae	5,480-02
34	24	2.3	1404	59	AT006A3A	Arabidopsis thaliana	5,480-02
35	24	2.3	1404	59	AT006A3A	Arabidopsis thaliana	5,480-02
36	24	2.3	1404	59	AT006A3A	Arabidopsis thaliana	5,480-02
37	24	2.3	1404	59	AT006A3A	Arabidopsis thaliana	5,480-02
38	24	2.3	1404	59	AT006A3A	Arabidopsis thaliana	5,480-02
39	24	2.3	1404	59	AT006A3A	Arabidopsis thaliana	5,480-02
40	24	2.3	1404	59	AT006A3A	Arabidopsis thaliana	5,480-02
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ALIGNMENTS

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32

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NRD	q1212780
REFERENCE	Walters, W. A. 1997. <i>Journal of Ecology</i> 85: 1001-1011.
SOURCE	leafy mustard.
ORIGINISM	Brassicaceae juncea

REFERENCE	TITLE
1 (bases 1 to 1381)	ADP-glucose pyrophosphorylase small subunit cDNA from <i>Arabidopsis thaliana</i>
Chem, B. Y. and James, H. W.	

JOURNAL
Plant Physiol. 109, 1498-1498 (1995)
REFERENCE
Z (bases 1 to 1381)

TITLE	Direct Submission
JOURNAL	Suppl. 1-4 (19 Nov. 1950) 1-12, 13-16, 17-18, 19-20, 21-22, 23-24, 25-26, 27-28, 29-30, 31-32, 33-34, 35-36, 37-38, 39-40, 41-42, 43-44, 45-46, 47-48, 49-50, 51-52, 53-54, 55-56, 57-58, 59-60, 61-62, 63-64, 65-66, 67-68, 69-70, 71-72, 73-74, 75-76, 77-78, 79-80, 81-82, 83-84, 85-86, 87-88, 89-90, 91-92, 93-94, 95-96, 97-98, 99-100, 101-102, 103-104, 105-106, 107-108, 109-110, 111-112, 113-114, 115-116, 117-118, 119-120, 121-122, 123-124, 125-126, 127-128, 129-130, 131-132, 133-134, 135-136, 137-138, 139-140, 141-142, 143-144, 145-146, 147-148, 149-150, 151-152, 153-154, 155-156, 157-158, 159-160, 161-162, 163-164, 165-166, 167-168, 169-170, 171-172, 173-174, 175-176, 177-178, 179-180, 181-182, 183-184, 185-186, 187-188, 189-190, 191-192, 193-194, 195-196, 197-198, 199-200, 201-202, 203-204, 205-206, 207-208, 209-210, 211-212, 213-214, 215-216, 217-218, 219-220, 221-222, 223-224, 225-226, 227-228, 229-230, 231-232, 233-234, 235-236, 237-238, 239-240, 241-242, 243-244, 245-246, 247-248, 249-250, 251-252, 253-254, 255-256, 257-258, 259-260, 261-262, 263-264, 265-266, 267-268, 269-270, 271-272, 273-274, 275-276, 277-278, 279-280, 281-282, 283-284, 285-286, 287-288, 289-290, 291-292, 293-294, 295-296, 297-298, 299-300, 301-302, 303-304, 305-306, 307-308, 309-310, 311-312, 313-314, 315-316, 317-318, 319-320, 321-322, 323-324, 325-326, 327-328, 329-330, 331-332, 333-334, 335-336, 337-338, 339-340, 341-342, 343-344, 345-346, 347-348, 349-350, 351-352, 353-354, 355-356, 357-358, 359-360, 361-362, 363-364, 365-366, 367-368, 369-370, 371-372, 373-374, 375-376, 377-378, 379-380, 381-382, 383-384, 385-386, 387-388, 389-390, 391-392, 393-394, 395-396, 397-398, 399-400, 401-402, 403-404, 405-406, 407-408, 409-410, 411-412, 413-414, 415-416, 417-418, 419-420, 421-422, 423-424, 425-426, 427-428, 429-430, 431-432, 433-434, 435-436, 437-438, 439-440, 441-442, 443-444, 445-446, 447-448, 449-450, 451-452, 453-454, 455-456, 457-458, 459-460, 461-462, 463-464, 465-466, 467-468, 469-470, 471-472, 473-474, 475-476, 477-478, 479-480, 481-482, 483-484, 485-486, 487-488, 489-490, 491-492, 493-494, 495-496, 497-498, 499-500, 501-502, 503-504, 505-506, 507-508, 509-510, 511-512, 513-514, 515-516, 517-518, 519-520, 521-522, 523-524, 525-526, 527-528, 529-530, 531-532, 533-534, 535-536, 537-538, 539-540, 541-542, 543-544, 545-546, 547-548, 549-550, 551-552, 553-554, 555-556, 557-558, 559-560, 561-562, 563-564, 565-566, 567-568, 569-570, 571-572, 573-574, 575-576, 577-578, 579-580, 581-582, 583-584, 585-586, 587-588, 589-590, 591-592, 593-594, 595-596, 597-598, 599-600, 601-602, 603-604, 605-606, 607-608, 609-610, 611-612, 613-614, 615-616, 617-618, 619-620, 621-622, 623-624, 625-626, 627-628, 629-630, 631-632, 633-634, 635-636, 637-638, 639-640, 641-642, 643-644, 645-646, 647-648, 649-650, 651-652, 653-654, 655-656, 657-658, 659-660, 661-662, 663-664, 665-666, 667-668, 669-670, 671-672, 673-674, 675-676, 677-678, 679-680, 681-682, 683-684, 685-686, 687-688, 689-690, 691-692, 693-694, 695-696, 697-698, 699-700, 701-702, 703-704, 705-706, 707-708, 709-710, 711-712, 713-714, 715-716, 717-718, 719-720, 721-722, 723-724, 725-726, 727-728, 729-730, 731-732, 733-734, 735-736, 737-738, 739-740, 741-742, 743-744, 745-746, 747-748, 749-750, 751-752, 753-754, 755-756, 757-758, 759-760, 761-762, 763-764, 765-766, 767-768, 769-770, 771-772, 773-774, 775-776, 777-778, 779-780, 781-782, 783-784, 785-786, 787-788, 789-790, 791-792, 793-794, 795-796, 797-798, 799-800, 801-802, 803-804, 805-806, 807-808, 809-810, 811-812, 813-814, 815-816, 817-818, 819-820, 821-822, 823-824, 825-826, 827-828, 829-830, 831-832, 833-834, 835-836, 837-838, 839-840, 841-842, 843-844, 845-846, 847-848, 849-850, 851-852, 853-854, 855-856, 857-858, 859-860, 861-862, 863-864, 865-866, 867-868, 869-870, 871-872, 873-874, 875-876, 877-878, 879-880, 881-882, 883-884, 885-886, 887-888, 889-890, 891-892, 893-894, 895-896, 897-898, 899-900, 901-902, 903-904, 905-906, 907-908, 909-910, 911-912, 913-914, 915-916, 917-918, 919-920, 921-922, 923-924, 925-926, 92

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Glycyne.

1 (bases 1 to 1556)

AUTHORS Jeffery, E.P., Kinney, A.J., Gentry, K.L. and M.J.G.H.

TITLE Developmental and growth temperature regulation of two different
microsomal omega-6 desaturase genes in soybeans

JOURNAL Plant Physiol. 110 (1), 311-319 (1996)

MEEDLINE 96151506

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Chlorophyll *Embryophyta* group; Embryophyta, Magnoliopsida,
Magnoliopsida, Rutaceae, Sapindales, Falcaceae, Euphorbiaceae,
Glycyne.

1 (bases 1 to 1556)

AUTHORS Jeffery, E.P., Kinney, A.J., Gentry, K.L. and M.J.G.H.

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Glycyne.

1 (bases 1 to 1556)

AUTHORS Jeffery, E.P., Kinney, A.J., Gentry, K.L. and M.J.G.H.

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23

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Release 2007/01/16, FBI, Dallas, Re-opening Request Denied.
Copyright (c) 1993, 1994, 1996 by Joseph J. Felt, Jr., et al.
Distribution rights by IntelliConnect, Inc.

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1. The first group of respondents (n = 10) was composed of individuals who had been involved in a romantic relationship for a minimum of 12 months and had been together for a minimum of 6 months. The second group (n = 10) was composed of individuals who had been involved in a romantic relationship for a minimum of 12 months and had been together for a minimum of 6 months. The third group (n = 10) was composed of individuals who had been involved in a romantic relationship for a minimum of 12 months and had been together for a minimum of 6 months. The fourth group (n = 10) was composed of individuals who had been involved in a romantic relationship for a minimum of 12 months and had been together for a minimum of 6 months. The fifth group (n = 10) was composed of individuals who had been involved in a romantic relationship for a minimum of 12 months and had been together for a minimum of 6 months. The sixth group (n = 10) was composed of individuals who had been involved in a romantic relationship for a minimum of 12 months and had been together for a minimum of 6 months. The seventh group (n = 10) was composed of individuals who had been involved in a romantic relationship for a minimum of 12 months and had been together for a minimum of 6 months. The eighth group (n = 10) was composed of individuals who had been involved in a romantic relationship for a minimum of 12 months and had been together for a minimum of 6 months. The ninth group (n = 10) was composed of individuals who had been involved in a romantic relationship for a minimum of 12 months and had been together for a minimum of 6 months. The tenth group (n = 10) was composed of individuals who had been involved in a romantic relationship for a minimum of 12 months and had been together for a minimum of 6 months.

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Parti

Statistics: Mean 11.101; Variance 4.537; scale 2.44

Fred No. is the number of results produced by item i to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

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4	430	41.2	1472	65	SP012015	C. communis malic enzyme	0.00e+00
5	431	41.5	1453	67	COYMOED	C. communis malic enzyme	0.00e+00
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7	422	39.8	1449	64	PR000324	R. glutinis malic enzyme	2.00e-04
8	123	10.6	1110	62	LEVE01193	Lesquerella mRNA for malic enzyme	1.56e-08
9	40	5.2	1515	61	043688	Wheat malic enzyme	1.00e-28
10	39	3.4	1308	45	PF08411	Rice malic enzyme 1	3.22e-11
11	38	3.3	1208	17	058411	Rice malic enzyme 1	3.22e-11
12	28	3.3	1622	67	01025817	Sesamum indicum malic enzyme	1.91e-10
13	37	3.2	215	4	040078	Arabidopsis thaliana malic enzyme	1.11e-04
14	33	2.9	1333	68	01040001	V. vinifera malic enzyme	1.04e-05
15	33	2.9	1366	68	T0001903	Tobacco leaf malic enzyme	1.04e-06
16	33	2.8	1516	61	PF08345	Malic enzyme from Arabidopsis thaliana	5.42e-06
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18	30	2.6	1391	37	CE0147	Geneticist's reference strain	1.30e-04
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20	30	2.6	1606	61	E09979	Phytophthora infestans	1.30e-04
21	29	2.4	4444	61	PF018181	Rice glutamate decarboxylase	1.30e-04
22	29	2.5	1336	60	BNAL003A	Blasivora nigris lincolniae	6.71e-04
23	29	2.5	1505	59	AT000804	Arabidopsis thaliana	6.71e-04
24	29	2.5	1631	59	AT000801	Arabidopsis thaliana	6.71e-04
25	29	2.5	1797	61	PF059477	Pectin lyase from Arabidopsis thaliana	6.71e-04
26	28	2.4	1330	59	AT000800	Arabidopsis thaliana	3.16e-03
27	28	2.4	1409	59	AT000802	Arabidopsis thaliana	3.16e-03
28	28	2.4	1505	59	AT000800	Arabidopsis thaliana	3.16e-03
29	28	2.4	1672	60	AT000801	Arabidopsis thaliana	3.16e-03
30	33	3.3	1725	60	043688	Synonym: malic enzyme	1.44e-02
31	27	2.3	1400	20	000043	Synonym: malic enzyme	1.44e-02
32	26	2.2	1400	20	000043	Synonym: malic enzyme	6.34e-02
33	26	2.2	1400	20	000043	Synonym: malic enzyme	6.34e-02
34	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
35	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
36	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
37	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
38	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
39	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
40	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
41	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
42	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
43	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
44	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
45	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
46	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
47	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
48	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
49	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01
50	26	2.2	1728	47	00000000	Malic enzyme	2.32e-01

ALIGNMENTS

RESULT	1
LOCUS	POTASSIUM
DEFINITION	1361 bp cDNA K. pneumoniae mRNA for oleate desaturase.
DATE	25-MAY-1996

[illegible]

Search completed: Wed Dec 17 15:03:29 1997
Job time : 1605 secs.

Dy	835	TGCTACTCATACAGATTCAGTGGCAGCAAGAAATGCATTGTGAAGGACAATTTCCATAACCGTTC	894
Jb	478	GACGAGAGATCTATGAGATCTGTTGATGCGAGTGATTCAGCTTAAGCTCAAGACGCCGACGACGGAGA	537
Oy	899	CATGAGAACATCAAGAAATCTTAAA/AAGGCTCTTTC/TAAATATATTC/CATATCA/GAAGCTGGCC	954
Jb	538	cacca 542 II II	
Oy	955	CATCA 959	
RESULT 9			
ID	TZ7012 standard; cDNA; 543 BP.		
AC	TZ7012;		
DE	10-SEP-1996 (first entry)		
KM	Kappa family acid hydroxylase clone plesq2.		
KM	Kappa family acid hydroxylase Lesquerelle acid transgenic plants;		
KM	sulfowest seed oil; tobacco; Genetic Resources Center, Kansas State		
KM	sulfowest sulfowest cottonseed, soybean, peanut, coconut,		
KM	oil palm; corn; ss.		
FH	Lesquerella fendleri.		
FH	Key Lesquerella fendleri		
FT	misc_difference 83		
FT	/tagr "a		
FT	/more "Base n at position 83 is not identified"		
FN	M0941007S-AI.		
FD	04-APR-1996.		
FE	25-SEP-1995 0110000.		
FR	26-SEP-1994 US 314596.		
FR	11-OCT-1994 US 345982.		
FR	29 SEP 1995 US 429982.		
PA	(BR00/) BROUN P.		
PA	(SOME/) SOMERVILLE C.		
FA	(VLD0/) VAN DE LOO F J.		
E1	Breun B., Somerville C., Van De Loos B.;		
DR	MF1_96-200914/20.		
PT	Prodn. of hydroxylated fatty acids, e.g. trihydroxy-L-hydroperoxide		
PT	acid - in genetically modified plants such as rapeseed, flax,		
PT	sunflower or cotton, cont. a fatty acid hydroxylase gene.		
PS	Claim 4; Page 65 66; 10pp; English.		
CC	cDNA clones plesq2 (#77012) and plesq3 (#Z7013) were obsd. from a		
CC	Lesquerella fendleri library by PCR amplification using primers		
CC	(see also #P00911). Found no overlap of homology between sister Luffs		
CC	hydroxylase and the Arabidopsis delta desaturase (#241). The genes		
CC	crossing-linkage are highly and specifically expressed in		
CC	seeds of L. fendleri. A genomic clone, plesq Hyd (#Z7011), was		
CC	isolated using plesq2 as probe, and shown to encode a kappa family		
CC	acid hydroxylase (#87039). Transgenic plants that express plesq2		
CC	contain altered levels of hydroxylated fatty acids, e.g. lesquerellin		
CC	acid (14 hydroxy D-linolenic acid), lin seed oils, waxes and		
CC	related products.		
SQ	Sequence: 543 bp, 100 % 100 % 100 % 100 %		
Every Match:	22.9%, Exact 27%, EG 2% Length 15%		
Rust Local Similarity	76.8%, Rust Dist 1.4E+09%		
Matches 419, Conservative	% Mismatches 122% Indels 3% Gaps 1%		
Dy	7	CACCAGTAGGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGAC	66
Oy	421	CATPCCAAGCAATTCGACGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGAC	486
Jb	67	AAGAGAGAGTGAATGAGAGTGAATGAGAGTGAATGAGAGTGAATGAGAGTGAATGAGAGTGAATGAGAG	124
Oy	481	AAGAGAGTGAATGAGAGTGAATGAGAGTGAATGAGAGTGAATGAGAGTGAATGAGAGTGAATGAGAGT	646

Dh	127	ggttgaagttgagttgattacatccgggtggtggttgatctatggtttatgtatcaggtt	180
Dh	128	tttttttttttttttttttttttttttttttttttttttttttttttttttttttttt	181
Dh	541	attgtatcatcttctctctctctctctctctctctctctctctctctctctctctct	600
Dh	187	agagctatctgttgggttcttctctctctctctctctctctctctctctctctctct	243
Dh	601	acatttttttttttttttttttttttttttttttttttttttttttttttttttttt	660
Dh	244	ctgtgaagctctctctctctctctctctctctctctctctctctctctctctctctct	303
Dh	441	ctctctctctctctctctctctctctctctctctctctctctctctctctctctctct	720
Dh	304	tacgttttctgtctctctctctctctctctctctctctctctctctctctctctct	363
Dh	721	ttttttttttttttttttttttttttttttttttttttttttttttttttttttttt	780
Dh	364	ttttttttttttttttttttttttttttttttttttttttttttttttttttttttt	423
Dh	781	ttttttttttttttttttttttttttttttttttttttttttttttttttttttttt	840
Dh	424	ttttttttttttttttttttttttttttttttttttttttttttttttttttttttt	483
Dh	841	ttttttttttttttttttttttttttttttttttttttttttttttttttttttttt	900
Dh	484	ttttttttttttttttttttttttttttttttttttttttttttttttttttttttt	542
Dh	901	ttttttttttttttttttttttttttttttttttttttttttttttttttttttttt	959
Dh	941	ttttttttttttttttttttttttttttttttttttttttttttttttttttttttt	999
RESULT	10		
IC	066072	standard; cDNA; 673 BP.	
AD	066072:		
DT	09-NOV-1994	(first entry)	
DE	Cloning of a cDNA encoding a delta-12 desaturase in the DNA of		
DE	plasmid pRF2.1C.		
KW	Fatty acid; desaturase; lipid; unsaturated; transgenic plant; ss.		
CS	Ruminant community.		
FT	key	transcription	
FT	CDS	1..673	
FT	/flag: a		
FN	M0941516-A.		
FN	26 MAY 1994.		
PF	15-OCT-1993; 009487.		
PP	10-SEP-1993; 00607336		
PA	(mpo) DU PONT DE NEMOURS & CO E. I.		
PI	digestion pf, deoxy 10/		
PI	wt: 3438255/22.		
PR	p pS08; pS4011.		
PR	Cloning of a cDNA encoding a delta-12 desaturase in the DNA of		
PR	plasmid lipid composition		
PR	Cloning of a cDNA encoding a delta-12 desaturase in the DNA of		
PR	plasmid lipid composition		
CC	Polysomal mRNA was isolated from castor beans of stages 1-11 (5		
CC	to 10 d) of each mRNA was used for synthesis pm PCR reactions.		
CC	The reverse transcriptase reaction was primed with random		
CC	hexamers and the PCR reaction with degenerate delta-12		
CC	desaturase primers NPT and NPT2 (Kobayashi, 1990). A DNA fragment		
CC	of approx. 700 bp was amplified from both stage 1-11 and stage		
CC	IV mRNA. The amplified DNA fragment from one of the reactions		
CC	was gel purified and cloned into a vector to create plasmid		
CC	pRF2.1C. The 100 bp insert in pRF2.1C was sequenced (GenBank).		
CC	An isolated nucleic acid fragment wherein the nucleic acid identity		
CC	is not equivalent to sequence G66071 is claimed. A method to		

[illegible][illegible]

CC	isolate/nucleic acid fragments encoding fatty acid desaturases
CC	and related enzymes is claimed which comprises: comparing AA
CC	sequences in R03697-R03782 and other fatty acid desaturase sequences;
CC	identifying conserved sequences of 4 or more bases designated hereinafter
CC	oligos based on the conserved sequences; and using the oligos to
CC	isolate sequences encoding fatty acid desaturases and
CC	desaturase-related enzymes.
CC	Sequence 673 BP; 154 A; 169 C; 150 G; 200 T;
CC	Query Match 72.38; Size 657; DB 10; Length 673;
CC	Best Local Similarity 70.38; Pos. No. 1,324-166;
CC	Matches 471; Conservative 0; Mismatches 166; Indels 3; Gaps 2;

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20

AC	Q19572;		(first entry)
DT	89-APR-1991		
DE	Human Natriuretic Peptide Receptor B.		
EW	M629; A297; M97; CNGC; kidney failure; heart failure; hypertension; hypotension; glucocorticoid therapy; glycine		
KW	hypertensive disease; glaucoma; gonorrhea; glycosylase		
OC	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..22	
ET	/label= signal sequence		
ET	Protein	12	
FT	/label= mature NPBR	23..495	
FT	Tetramer		
ET	/label= extracellular domain		
FT	/note= "binds natriuretic peptides A,B and C"		
FT	Domain	456..496	
FT	/label= transmembrane domain		
ET	Domain	479..1047	
FT	/label= cytoplasmic domain		
FT	/note= "GC and protein kinase activity"		
ET	Modified site:	24..26	
ET	/label= N-glycosyl site		
ET	Modified site:	35..37	
ET	/label= N-glycosyl site		
ET	Modified site:	161..163	
ET	/label= N-glycosyl site		
ET	Modified site:	195..197	
ET	/label= N-glycosyl site		
ET	Modified site:	244..246	
ET	/label= N-glycosyl site		
ET	Modified site:	277..279	
ET	/label= N-glycosyl site		
ET	Modified site:	321..331	
ET	/label= N-glycosyl site		
ET	Modified site:	600..602	
ET	/label= N-glycosyl site		
PN	UniProt/Q2-A-		
PD	10-JAN-1991.		
PF	ZZ-MIN-1990; 1103586.		
PR	ZZ-MIN-1989; HS 370673.		
PA	(GSTR) GENOSCREEN INC.		
P1	Chang M, Goodall D, Lowe J;		
DR	WPLJ; 91-036711/05.		
NL	N-PDBB; Q10324.		
PT	Natriuretic peptide receptor B = for diagnosis and treatment of		
PT	kidney failure, heart failure, hyperaldosteronism, glaucoma etc.		
CS	Claim 3; Fig 1; 49pp; English.		
CC	The sequence was derived from the cDNA encoding natriuretic peptide		
CC	receptor B, being having propeptidylglycylase (GP) activity and protein		
CC	kinase activity. The DNA can be inserted into expression vectors		
CC	for the production of the protein, opt. after being mutated to produce		
CC	NNPB analogues. The protein has a mol wt. of 115 kd (calculated Mr		
CC	114,973). The protein (or variants) can be used in treatment of		
CC	natriuretic peptide disorders, and also to isolate peptides using		
CC	affinity chromatography. Antibodies with affinity for NPBR can		
CC	also be prepd.		
SQ	Sequence: 1047 BP, 67 A, 15 C, 83 G, 13 T,		
GB	GenBank Match:	8.4%	Coverage: 95% CB Z Length 1047
	Best Local Similarity:	8.8%	Pred. No. 1,776-47
Matches	63; Conservative 271; Misses 577; Indels 10; Gaps 8;		
Dn	49 v unvunatg gnnv dnt vnssngagcsnygnamsavdknhkhdhknmgqevyvasv		108
At	: : : : : : : : : : : : : : : :		:
Gp	gggtatttgcctccacttcacaaaccgatcatcgaggcccttgcttatctttgaatacaattcca		926

[illegible]

AC	0105722	
PT	09-APR-1991	(first entry)
DE	Human Natriuretic Peptide Receptor B.	
SM	NPBR; ANP; ANP; NP; kidney failure; heart failure; protein kinase; hyperaldosteronism; glaucoma; guanylyl cyclase.	
CC	mem systems.	
FT	Key	location/qualifiers
FT	Peptide	1..22
FT	/label= signal sequence	
FT	Protein	12
FT	/label= mature NPBR	
FT	Domain	23..455
FT	/label= extracellular domain	
FT	/note= "binds natriuretic peptides A,B and C"	
FT	Domain	456..456
FT	/label= transmembrane domain	
FT	Domain	479..1047
FT	/label= cytoplasmic domain	
FT	/note= "30 and protein kinase activity"	
FT	Modified-site	24..26
FT	/label= N-glycos site	
FT	Modified-site	35..37
FT	/label= N-glycos site	
FT	Modified-site	161..163
FT	/label= N-glycos site	
FT	Modified-site	195..197
FT	/label= N-glycos site	
FT	Modified-site	244..246
FT	/label= N-glycos site	
FT	Modified-site	277..279
FT	/label= N-glycos site	
FT	Modified-site	349..351
FT	/label= N-glycos site	
FT	Modified-site	600..602
FT	/label= N-glycos site	
FN	W09100792 A.	
PD	10-JAN-1991	
PF	22-JUN-1990	003586.
PR	23-JUN-1989	US 370673.
PA	(GSTR.) GENENTECH INC.	
P1	Chang M, Goeddel D, Lowe D	
P1	WPI; 91-036711/05.	
DR	N-PSDB; 010324.	
PT	Natriuretic protein receptor B for diagnosis and treatment of	
PT	kidney failure, heart failure, hyperaldosteronism, glaucoma etc.	
P3	Claim 3, Fig 1; 1990 English.	
CC	The sequence was derived from the DNA encoding natriuretic peptide	
CC	receptor B, cDNA, having high catalytic (65) activity and protein	
CC	kinase activity. The DNA can be inserted into expression vectors	
CC	for the production of the protein, after being modified to produce	
CC	NPBR analogues. The protein has a mol wt of 114 kD (calculated Mw	
CC	114,070). The protein (or variants) can be used in treatment of	
CC	natriuretic peptide disorders, and also to isolate peptides using	
CC	affinity chromatography. Antibodies with affinity for NPBR can	
CC	also be prepared.	
CC	sequences: ind 1; 2; 3; 4; 5; 6; 7; 8; 9; 10; 11;	

RESULT 12
ID Q10512 STANDARD; DNA; 100% GP.

[illegible]

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23

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24

Dc	362	maknchdnt flwvwr an phdch b h a n s y s t e m i s k h e w g r i m w e y g a n s d h o n e 444
Yy	470	TTTCCCTCAAGAAAGGTATATAATCAATGCTACGGTAAGTACTTAAACCACTTTGCG 529
Dc	441	ndhdhscckklnsthravwvofygtl rrmogvssstnnt klnntkvnssmwtl r w l n 494
Yy	530	GATTAATACATTAAGTAAAGCTTAATTAATTAATGATTAAGCTTAAGCTTAATTAATTA 584
Dc	500	agssv yk h a y s t a t i s s u s g s y s t e m i s h y k u n t a n t g h a p v a c k l n k h n 558
Yy	590	ACCTCTGCGAAACCTTACCAACCGGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTCA 649
Dc	559	ntlrnrmnckhr dvnantht lmgxndnmccvrtlycn gsnthkndndnmckm 618
Yy	660	TTCTATACATTAAGTAAAGCTTCTTAATATATATATATATATATATATATATATATATAT 708
Dc	619	nysnmndvkmnhbnsnshbysksncvdslnvknkdygnastlannndn 678
Yy	709	TGTAATGCTTCTTCCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 767
Dc	679	anyaknntannnsqnnnrtgmaadvyngnnnnnanzsgnyuynshnknnv 738
Yy	768	CGAATGCTTCCTTCTTATTTTAAATGCTTCCTTCTTCCTTCTTCTTCTTCTTCTTCTTCT 817
Dc	739	kvtngnrygnnsdrtnnnnnnnnnmrcwzndhantdognnkgnnt rnkngyrt ssa 798
Yy	828	CTATCTTCCTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 887
Dc	794	dnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 854
Yy	888	TAACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 937
Dc	859	svtngnsdygnlansnsttmnnyvnmndyrtendndnddykwt rggzayvysgn 919
Yy	948	CTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1007
Dc	919	ngnngnrtannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 977
Yy	1008	ATATAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1066
Dc	978	engdtvntastmssngnkhvscrtkrdndngnsmnngzgmkykknrtlymna 1037
Yy	1067	CTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1125
Dc	1038	gnkgy 1042
Yy	1127	GTCTG 1131

D8	MPI_93376864/48.
Pt	New oligonucleotide probes specific for Mycobacterium used for detection and amplification of Mycobacteria nucleic acid in PT samples
PS	Claim 3; Page 14; 23pp; English.
Cc	Oligonucleotide probe MK14 A consists of nucleotides 5'-95' of MK14 CQ(051735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection.
CC	See also Q51735-45 and Q51747-59.
Sq	Sequence 91 Br; 5 A; 17 G; 15 G; 4 T;
Db	A teegagssvshyywoshahwhhvhhvhvvsvvghlvghvghgghgvysvc 60 : :: :: :: :: :: :: :: :: :: :: :: :: Gcg gctgcattatcatcaacaaaccgttaaacpaacaataccacttcaga cttc
Gy	bcm pncfrraatlpttacccaacacgaaggaaaacgggcccccccacga ctg
RESULT 14	
ID	Q51746 standard; cDNA; 91 BP.
An	Q51746;
DT	31-MAY-1994 (first entry)
DE	Oligonucleotide probe MK14 A
KM	Oligonucleotide; DNA primer; mycobacterial disease diagnosis?
XW	ss.
OS	Synthetic.
PN	FP-571911-A. P1-OEY-1993.
PD	01-JEN-1993.
FZ	24 Mar 1993; 106725.
PR	26-MAY 1994; US-884651.
PA	(BEST) REPTON MYRINSON CO
EI	Shank DG, Spears PA; MPI_93376864/48.
PT	New oligonucleotide probes specific for Mycobacterium used for detection and amplification of Mycobacteria nucleic acid in PT samples
ES	Claim 3; Page 14; 23pp; English.
CC	Oligonucleotide probe MK14 A consists of nucleotides 5'-95' of MK14 CQ(051735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection.
CC	See also Q51735-45 and Q51747-59.
Sq	sequence 91 Br; 5 A; 17 G; 15 G; 4 T;
Rn	Query Match 3.6%; Score 42; FR % Identity 91, Best Local Similarity 11.7% Pred.No. 1,136-11; Matches 7; Conservative 44; Mismatches 9; Indels 0; Gaps 0;
CP	HUO tccatcttaaATAAGAAATACCTTGGATTGTCAACAACGCATTAACAAGCGAGC 1047 ::::: :::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: HUU tccatcttaaATAAGAAATACCTTGGATTGTCAACAACGCATTAACAAGCGAGC 1047
RESULT 15	
ID	N81164 standard; DNA; 204 BP.
NT	N81164;
OT	08-NOV-1990 (first entry)
BE	Bases substituted E.coli beta-galactosidase alpha-fragment.
EC	E.coli bet galactosidase alpha-fragment; base substitutions; ss.
CS	Escherichia coli.
CH	key beta-lam/Galliers

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MPs' α = 0.05, β = 0.80, database search, using Smith-Matthews algorithm.

Run on: Wed Dec 17 17:27:33 1997, Master time 139.04 seconds

Tabular output not generated.

Title: SUS-08-077A 1

Decay: P1000	(A 1.00) 1.00 0.08 0.00 0.00 0.00
Perfect Score:	1.05
N.A. Sequence:	1 ATGGGCTGAGAGCTGAAAGAAAT.....GGTAAATTAATGAGGATATGGA 1110

Comp:	TACOMSTAT-ADM.
	TACOMSTAT-ADM.

Scoring table: **TABLE default**

References

14066 seqs, 378345 bases & 2 contigs.

Listing first 45 summaries

Database: n-gene000728

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Model: $Q, C^{\infty}(\mathbb{R}^n); V^{\infty}(\mathbb{R}^n); \Gamma(\mathbb{R}^n); \mathcal{S}(\mathbb{R}^n); \mathcal{S}'(\mathbb{R}^n); \mathcal{D}'(\mathbb{R}^n)$

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	Seq. ID
1	1082	43.7	134	10	G66069	Sequence encoding mtr 0.00+0.00
2	804	42.8	797	10	G66074	Sequence of microsome 0.00+0.00
3	804	42.6	131	10	G66068	Sequence encoding mtr 0.00+0.00
4	600	51.9	185	21	T73011	KP82 fatty acid synth 0.00+0.00
5	379	32.8	130	10	G66071	Sequence of mtr 0.00+0.00
6	334	29.4	142	10	G66070	Sequence encoding mtr 1.62+0.22

7	319	27.6	544.21	12793	KRPA1 (gtr) + 103 bp	3.43e-21
8	319	27.6	1599.10	946073	Sequence of carboxy-terminus	4.51e-18
9	280	24.2	563.41	127012	Kappa-lactamase from <i>Yersinia enterocolitica</i>	4.51e-18
10	267	23.1	618.10	646622	Sequence of carboxy-terminus	2.20e-17
11	110	8.7	1047.2	610572	Human Maltotetraose 6-phosphatase	1.99e-50
12	69	6.0	1647.7	610572	Human Maltotetraose 6-phosphatase	4.72e-29
13	47	4.1	91.9	651746	Oligonucleotide probe	1.39e-14
14	43	3.7	204.1	188116	3'ase substituted probe	4.42e-12
15	42	3.6	91.9	651746	Oligonucleotide probe	1.83e-11
16	39	3.4	204.1	188116	3'ase substituted probe	1.24e-09
17	38	3.3	114.12	670465	Genomic DNA sequence	4.94e-09
18	37	3.2	114.12	670470	Genomic DNA sequence	1.35e-08
19	36	3.1	114.12	670467	Genomic DNA sequence	7.65e-08
20	36	3.1	114.12	670473	Genomic DNA sequence	7.65e-08
21	35	3.0	114.12	670468	Genomic DNA sequence	2.96e-07
22	35	3.0	114.12	670469	Genomic DNA sequence	2.96e-07
23	35	3.0	114.12	670469	Genomic DNA sequence	2.96e-07
24	34	2.9	114.12	670471	Genomic DNA sequence	1.36e-06
25	34	2.9	114.12	670466	Genomic DNA sequence	1.13e-06
26	34	2.9	114.12	670466	Genomic DNA sequence	1.13e-06
27	33	2.9	114.12	670468	Genomic DNA sequence	4.22e-06
28	33	2.9	114.12	670468	Genomic DNA sequence	1.13e-06
29	34	2.9	114.12	670465	Genomic DNA sequence	1.13e-06
30	33	2.9	114.12	670470	Genomic DNA sequence	4.22e-06
31	33	2.9	114.12	670470	Genomic DNA sequence	4.22e-06
32	30	2.6	1429.7	243206	Sequence encoding P1b	2.13e-04
33	30	2.6	1429.7	243206	Sequence encoding P1b	2.13e-04
34	30	2.6	1429.7	243206	Sequence encoding P1b	2.13e-04
35	30	2.6	1429.7	243206	Sequence encoding P1b	2.13e-04
36	30	2.6	1429.7	243206	Sequence encoding P1b	2.13e-04
37	29	2.5	565.6	623532	HIV-1 gp120 and gp120	2.13e-04
38	28	2.4	39.7	651787	Mixed oligonucleotide	2.62e-04
39	28	2.4	39.7	651787	Mixed oligonucleotide	2.62e-04
40	28	2.4	39.7	651787	Mixed oligonucleotide	2.62e-04
41	28	2.4	39.7	651787	Mixed oligonucleotide	2.62e-04
42	28	2.4	39.7	651787	Mixed oligonucleotide	2.62e-04
43	28	2.4	39.7	651787	Mixed oligonucleotide	2.62e-04
44	28	2.4	39.7	651787	Mixed oligonucleotide	2.62e-04
45	27	2.3	146.21	113623	Genomic DNA sequence	9.20e-03

ALIGNMENT

RESULT	1
LD	466069 standard; 010NA; 1304 BP.
AC	Q66069;
DT	09 NOV-1994 (first entry)
PT	Comp. to existing literature; data is described in ref. 1
DE	CE2-165d.
KA	Patty acid, desaturase, lipid unsaturated, trans-unsaturated, ES
OS	Brassicaceae napus.
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	99..1250
FT	/*tag = a
PN	MO9411516-A.
PD	26 MAY-1994.
PR	15-OCT-1993; 104967.
PR	17 NOV-1992; US 9773339.
PA	(map) 100 POINT DE REPONSE 6 CO E. I.
PI	14th met. 4E, 0000000?
IN	WFL; 94.1845154/72.
IN	P-DS007; 853688.
FT	Gene for fatty acid desaturase enzyme - partial alteration of
FT	plant lipid composition

where in the nucleic acid identity is 90% or greater to Q65068 or Q65074 is claimed.

Query M. M. M. 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 8

Matches 300; Conservative 11; Mismatches 164; Indels 5; Gaps 7.

[illegible]

Ob 1719 ucaagugcgtgcgcctggagaaacgcgccttctctggctggggatctgaaagaaacatctc 1778
+ ||||| || || ||||| ||||| ||| || ||||| || ||||| ||| ||||| |||||
Nc 61 ATCAACGCGCTATCTGTAACAACGCGCGCTGATCTGTGTAACAATCAACAACATTAAT 159

DG 0796 GAGGGGTTGTCTTTCATCCTACCGTGCCCTC 1838
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 CCAAGATTAAATCTCATCTCTCTCTCTAATCTGCACACT 1840

[illegible][illegible][illegible][illegible][illegible]

461 AAGAACTCAACATCAAGTGGTAAAGTAACTAAACAACTTTGGACAAATGAG 546

49 ATTGTAACGCTTCACTTCTTCCGATTCGCTTAACTTCAAGCTCTTCCGCG 606
541 ATTGTAACGCTTCACTTCTTCCGATTCGCTTAACTTCAAGCTCTTCCGCG 606
585 ATTGTAACGCTTCACTTCTTCCGATTCGCTTAACTTCAAGCTCTTCCGCG 606

[illegible][illegible]

Db 2436 ctgatagtgaaatgcgttcctcgtcttgaacttaattgcaaacac;catccctcgltg 2495
||||| || ||||| ||||| || | ||||| ||||| ||||| ||||| || ||

Dec 17 17:24 /home/fuller/dec97/US-08-572-027A-7.mpg

9

[illegible]

DNA sequence analysis revealed that the cDNA sequence was identical to that of the rat *p70* gene [GenBank accession number U18696]. The nucleotide sequence of the cDNA was determined by primer extension from both ends of the PCR product. The sequence was confirmed by sequencing the PCR product directly.

[illegible][illegible]

D6 2735 1095g^a g' t' t' t' g' g' j g j g j g j g j g' g' g' a a g g g g g g g' t' t' t' a c g g' g' g' c 2789
|||||
|||
D7 1081 AAGGAAATGATTATTTTAAAAGGTAACAAAGGGGTACGGAATAAAGGCTGCTTGCTTGGGAT 1140
|||||

15	2706	1333+337+373	2810
Qy	1141	AA7AATTAACTTATCA	1155

RESULT	
IR	4666.66 standard; cDNA; 1372 BP.
AC	466068;

DE Sequence encoding microsomal delta-12 desaturase.
 FM Fatty acid; desaturase; lipid; unsaturated; transgenic plant; ss.
 OS *Arabidopsis thaliana*.

FT	CDS	93.124
FT	/★tag a	
PN	W09411516-A.	
mn	25-MV-180A	

PR 15-DEC-1983; 0009667.
 PR 17-NOV-1982; 03-977339.
 PA (DDPO) DU PONT DE NEMOURS & CO E. I.
 P1 Lightner JF, Oskley JJ;

PT Genes for fatty acid desaturase enzymes - permit alteration of plant lipid composition

The gene responsible for *zfx66b* was isolated by screening *Arabidopsis* genomic DNA library using radiolabeled pSF2b cDNA insert, purifying positively hybridizing plasmids, and subcloning a 6 kb Hind III insert

The sequences of the gene (*gkknk*) and the rDNA (*gkrksn*) revealed the presence of a single insertion of 1134 bp at a position between CC nucleotides 88 and 89 of the rDNA, which is 4 nucleotides 5' to the initiation point. The rDNA is contained in a linear dimeric plasmid molecule.

CC 066068 or 066074 is claimed.

Query Match	69.6%;	Score 804;	EB 10;	length 1372;
Best Local Similarity	85.5%;	Pred. No. 0.00e+00;		

[illegible][illegible]

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/home/fuller/dee97/US-08-572-027A-5.mg

15

Dh 528 catatggtttttagtgatcagctgggtgatgacatgttggtgattgtgacatct 479
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 325 CACCAAGCTTTTAAAGCTAAATATATATATATATATATATATATATATATAT 584
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 580 ggttttgggttttgggttttgggttttgggttttgggttttgggttttgggt 639
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 385 TTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 444
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 649 ggttttgggttttgggttttgggttttgggttttgggttttgggttttgggt 699
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 445 GGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 504
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 700 tctttagtctttagtctttagtctttagtctttagtctttagtctttagtctt 759
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 505 GGTAAATATATATATATATATATATATATATATATATATATATATATATAT 564
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 760 ggttttgggttttgggttttgggttttgggttttgggttttgggttttgggt 816
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 545 GGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 604
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 817 tgggtttgggttttgggttttgggttttgggttttgggttttgggttttgggt 876
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 625 TGTATATATATATATATATATATATATATATATATATATATATATATATAT 684
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 877 ggttttgggttttgggttttgggttttgggttttgggttttgggttttgggt 936
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 685 TGTAAATATATATATATATATATATATATATATATATATATATATATATAT 744
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 937 tgggtttgggttttgggttttgggttttgggttttgggttttgggttttgggt 996
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 745 GTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 804
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 997 atggtttggttttgggttttgggttttgggttttgggttttgggttttgggt 1056
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 805 TTGATATATATATATATATATATATATATATATATATATATATATATATAT 864
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 1057 ggttttgggttttgggttttgggttttgggttttgggttttgggttttgggt 1116
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 865 GATTTGTTTAAAGCTTTTAAAGCTTTTAAAGCTTTTAAAGCTTTTAAAGCT 924
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 1117 tttcatatcatgagacatcatgagacatcatgagacatcatgagacatcatg 1176
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 925 TTGAAATATATATATATATATATATATATATATATATATATATATATATAT 984
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 1177 catgcatggagacatggagacatggagacatggagacatggagacatggagac 1236
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 985 CATGATATATATATATATATATATATATATATATATATATATATATATATAT 1044
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 1237 ggttttgggttttgggttttgggttttgggttttgggttttgggttttgggt 1296
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 1045 GGTAAATATATATATATATATATATATATATATATATATATATATATATAT 1104
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 1297 ggttttgggttttgggttttgggttttgggttttgggttttgggttttgggt 1356
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 1105 CATATATATATATATATATATATATATATATATATATATATATATATATAT 1164
|| || || || || || || || || || || || || || || || || || || || || ||

RESULT 8
ID T27013 standard; cDNA; 544 BP.
AC T27013;
DT 10-SEP-1996 (first entry)
DE Kappa fatty acid hydroxylase; lesquerollic acid; transgenic plant;
KW Kappa fatty acid hydroxylase; lesquerollic acid; transgenic plant;

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/home/fuller/dee97/US-08-572-027A-5.mg

16

KM oilseed; seed oil; rapeseed; Canola; Brassica juncea (var.) flax;
KM sulfonol; sulfonol; cotton; rapeseed; soybean; peanut; coconut;
KM oil palm; corn ss.
NM Lesquerella fendleri.
PN M09610075-A1.
PD 04-APR-1996.
PP 25-SEP-1995; 011855.
PE 26-SEP-1994; 08-04346.
PR 11-OCT-1994; 08-320982.
PS 26 SEP 1995; 09 320982.
PA (BR01) BR01 P.
PA (SOME) SOMEVILLE C.
PA (VLOO) VAN DE LOO F.J.
PI Rapeseed, Canola, flax, Van De Loos B.J.
DR WPIJ 96-200914/20.
PT Fruits of hydroxylated fatty acids; high protein oil; lesquerollic
PT acid - in genetically modified plants such as rapeseed, flax,
PT sulfonol or cotton; cotton; a fatty acid hydroxylase gene
PS Claim 4; Page 66; 105pp; English.
XX CMA clones (1992) (T27013) and CMA3 (T27013) were obtained from a
OC Lesquerella fendleri library by PCR amplification using primers
OC (see also T27013-17) based on regions of homology between kappa
OC hydroxylase and Arabidopsis desaturase (14d). A genomic
OC clone, pKappa-14 (T27013), isolated using phage2 as probe, encoded a
OC kappa fatty acid hydroxylase (895579). Transgenic plants that express
OC pKappa-14 contain altered levels of hydroxylated fatty acids, e.g.
OC lesquerollic acid (14-hydroxy-11-tetradecenoic acid), in seed oils, waxes
OC and related products.
SQ Sequence 544 BP; 135 A; 153 C; 105 G; 161 T;

Query Match 27.6%; Score 319; LR 21; Length 544;
Fast Low Complexity 60.6%; E=0.0; 230 211;
Matches 440; Conservative 0; Mismatches 103; Indels 3; Gaps 1;

Dh 1 tataggacggagacatctaacacgggtggtggtggtggtggtggtggtggtggtggt 60
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 415 TATAGATATATATATATATATATATATATATATATATATATATATATATATAT 474
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 61 ccaagacggaatccgacatcgaatggtggtggtggtggtggtggtggtggtggtggt 120
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 475 CCCAGAGCAAGATACATATAGTGGTACGGCAATACGAAATGCAATGCAATGCAAT 534
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 121 atcatgatttaattggtggtggtggtggtggtggtggtggtggtggtggtggtggt 180
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 535 ACCGATATATATATATATATATATATATATATATATATATATATATATATAT 594
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 181 tatgagacatcgaatggtggtggtggtggtggtggtggtggtggtggtggtggt 237
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 595 TGTAAATATATATATATATATATATATATATATATATATATATATATATATAT 654
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 228 aagagacggtgagacatcgaatggtggtggtggtggtggtggtggtggtggtggt 297
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 655 AATGACGATATATATATATATATATATATATATATATATATATATATATATATAT 714
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 298 ggttttgggttttgggttttgggttttgggttttgggttttgggttttgggt 357
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 715 GGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 774
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 358 cgggtttggttttgggttttgggttttgggttttgggttttgggttttgggtttt 417
|| || || || || || || || || || || || || || || || || || || || || ||
Qy 775 CCGCTTTTAAATATATATATATATATATATATATATATATATATATATATATATAT 834
|| || || || || || || || || || || || || || || || || || || || || ||
Dh 418 ggttttgggttttgggttttgggttttgggttttgggttttgggttttgggtttt 477
|| || || || || || || || || || || || || || || || || || || || || ||

Db 277 chd1-nmynphhstqipsnrlkcyasicknwgelye 314
 E : |||| : || : || || || || :
 316 HMTDHWANRRCMNYNMRKRNKDLQK 349

RESULT	ENTRY	DATE
11	543772 #type complete Delta-12 desaturase Antibody variabilis #format_name Antibody variabilis #format_144 #format_144_144_144 #format_144_144_144 28-Oct-1994	19941028

Accessions	Reference
543772	
543770	
Authors	Journal
Sakamoto, M.; Wada, H.; Nishida, T.; Okamoto, M.; Morita, H.	Plant Mol. Biol. (1994) 24:643-650
Title	
Identification of genes involved in the pathogenicity of cyanobacteria.	

```
##accession 243772
##status preliminary
##residues 1-350 ##label 5MR
##length 350 ##molecular-weight 41283 ##checksum 73888
SUMMARY
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Query Match	6.43;	2,200,200;	18.16;	1,037.8;	350;
Best Local Similarity	27.35;	1,000,000;	2.15;	43;	
Matches	75;	Conservative	60;	Mismatches	113;
				Indels	71;
				Gaps	19;

D6 63 pmlplpwiftgltatgtfvahdcghrstakrwndvlgfimmllpyffswrwh 122
 : : | : | | : : | : : : : : : : : : : : :
 Q9 82 SYEAMFLYMAKQDVLDTQWVIMHEQLGPAFSLQGMILITGVTLTFSFLIIVYSWSWKEH 140

[illegible]

Dd 178 h-Id-wr-kikvkdq--ad-vklsvavv-vilaavipil-at-givgfvkfwfwm 227
:::|:::|:::|:::|:::|:::|:::|
Gy 201 ppygaafkrhshtnaalmhehdqlstsaalavvtatshyaaguvawmvrwvrrv 269

D6 228 lghfwmstftvwhtypdp-
feetvwheaaqglgllbodykawe
vlclnd-inviv 285

QY 461 livmeflvltlvmihrlslmldss-
wmtwzgal Alveedrgllnkrvf-
nnrtivw 377

Db 286 phlstaipynrlayessigenwdylh 314
 :ll :::l : - :l :l :
 QY 318 AHHEFSTMEHYHAMEATKRIIDGERTQ 316

RESULT	12
ENTRY	553300
	#+v1+comp1+e

FIELD NO.	DATE	ORGANISM	Local name	Scientific name	Common name
110	28-Oct-1996	Spinacia oleracea	Spinach	<i>Spinacia oleracea</i>	spinach

REFERENCE	553309
Schmidt, H.; Driesellhaus, T.; Buck, F.; Heinz, E. # Journal Plant Mol. Biol. (1994) 26:631-642	

title	Immigration and the Negro from Slavery to the Present
Accession	55369
status	preliminary

```

#residues      1 447 #residues
##cross-references EMBL:X78311
#length 447 #molecular weight 5306 #molecular mass 5306
SUMMARY

```

Query Match	8.4%	Score 255;	DB 16;	Length 447;
Best Local Similarity	20.5%	Info 0.00017023;		
Matches	81;	Conservative 64;	Mismatch 116;	Info 0.26;
				Caps 22;

[illegible][illegible]

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[illegible]

RESULT	13
ENTRY	S49331
	#type=complete

```

ORGANISM:
DATE:
#Initial name Spinach taken from #Text = text_spinach
#6 Feb 1995 #14 49:55 #next = 10 May 1995 #next_change
12-May-1995

```

REFERENCE
S49331
#authors
Schmidt, H.
#submission submitted to the EMBL Data Library, March 1994

```
##status      preliminary
##molecule_type mRNA
##residues    1-447 ##label SCH
```

Query Match	Length	Molecular-weight	Lengthsum
8.6%; Score 243; DB 10; length 447;	447	5143	6764

Db 127 wctvl|svt-a|a|f|mkapwv|l-plawar|ataltat|v|q|p|c|ah|s|f|s|k|n|l 1833
best local similarity 47.06; EICL No. 2036 at
Matches 60; Conservative 49; Mismatches 116; Indels 76; Gaps

58 MOLLASITZKATTEPILHHSSTAMPFMAVGVITGVVANSCHHESEYOM 117

118 LEEVVO LIIHELLEVEFWYCHKCHMSHTOSTEETEEVATTEGEOEHWYCHYLANDL 176

[illegible][illegible]

Dec 17 11:02 /home/fulher/dec97/US-08-572-027A-2.rpr

Query Match	8.4%	Score 255;	DB 16;	Length 447;
Best Local Similarity	20.5%	Info 0.00017023;		
Matches	81;	Conservative 64;	Mismatch 116;	Info 0.26;
				Caps 22;

[illegible][illegible]

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[illegible]

RESULT	13
ENTRY	S49331
	#type=complete

```

ORGANISM:
DATE:
#Initial name Spinach taken from #Text = text_spinach
#6 Feb 1995 #14 49:55 #next = 10 May 1995 #next_change
12-May-1995

```

REFERENCE
S49331
#authors
Schmidt, H.
#submission submitted to the EMBL Data Library, March 1994

```
##status      preliminary
##molecule_type mRNA
##residues    1-447 ##label SCH
```

Query Match	Length	Molecular-weight	Lengthsum
8.6%; Score 243; DB 10; length 447;	447	5143	6764

Db 127 wctvl|svt-a|a|f|mkapwv|l-plawar|ataltat|v|q|p|c|ah|s|f|s|k|n|l 1833
best local similarity 47.06; EICL No. 2036 at
Matches 60; Conservative 49; Mismatches 116; Indels 76; Gaps

58 MOLLASITZKATTEPILHHSSTAMPFMAVGVITGVVANSCHHESEYOM 117

118 LEEVVO LIIHELLEVEFWYCHKCHMSHTOSTEETEEVATTEGEOEHWYCHYLANDL 176

[illegible][illegible]

Dec 17 11:02

296 A-TVDRDYGLNKF-HNITDTHVHHHFFSTHMTNAMEATNAKPI LSEY 344

PROBATION	14	
ENTRY	55459	#type complete
TIME	Delta 32:28:49 (w/ 11.00)	Gravimetric loss of
ORIGIN	Formal name Special Physics	
DATE	08-Jul-1995	Temperature measured at Jul 1995 from "hang

ACCEPTED	554259
REFERENCE	554259
Authors	Mutata, N.; Deshimum, P.; Tazaka, Y.

submission submitted to the EMBL Data Library, April 1995
 # description Biosynthesis of gamma- lipoic acid in the cyanobacterium *Spirulina platensis*.
 # accession 514259

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preliminary
#status
#molecule_type DNA
#residues 1351
#cross_references EMBL:AB6736
oxidoreductase
#length 351
#molecular_weight 40028
#aminoacids 639
KEYWORDS
SIMILAR

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Query Match 7.8%; Score 236; DN 9; Length 351;
Best local Similarity 27.0%; Pred. No. 2,936 20;
Matches 73; Conservative 44; Mismatches 106; Indels 25; Gaps 20;

D6 66 PMLIPVWVIGTALQITIVRHDGQRSTSNMWNWDWGHLLFPLIY-PHSWG 174
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D7 87 SFAMLYAACGVLLPGVMIAHECHAFSGIRLDTVS LIFSELLVTFSWTS 140

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Db 125 hmqhkytneIdnaqpwkeeyqzqkfmqyldffgwwigsllhw-sinf-182
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Gy 141 HSHHSHTGSLSEDEYVFKSSQKMKGRKLA S FLATVQVLTVOFTLSMVTLENTV 190

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Db      183 wtk-ieg k.q rgyk tss lv lgaai-a-fpmitlq--vwtjtkiwi 2277
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Dy      194 GPPFVWGHKCHHNAATVNIHDKVYLVAAATLAVYVTFVYAAAGVAAWVTFV 2588

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Db      228  PAVIIVLWMSKILLNV LADIPISQVWYDSQSLGIDNYSWGFQADI  GKH 2866
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Dy      259  PLINVEGVLT LQNHFLHLLSNNMWSGLA YNLSVIGLVKE INITTH 156

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Db 287 alphavetaipwmlrtpwyzkagjely 316
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Qv 317 VAHHFSTMPHYHAMEATKAIKINSEY Y 345

ENTRY	RESULT
543770	15
Delta-12 desaturases	type complete
Synchocystis sp. (PCC6714)	
formal name: Synchocystis sp. (common name: PCC6714)	
26-Oct-1994	26-Oct-1994
20-Oct-1994	20-Oct-1994

ACCESSIONS	543770
REFERENCE	543770
#authors	Sakamoto, T., Wada, H., Nishida, I., Ohnori, M., Murata, N.
#journal	Plant Mol. Biol. (1994) 24:643-650
#title	Identification of conserved domains in the Pata 12 desaturases of cyanobacteria.
#accession	543770
#status	preliminary
#residues	1 349 ##label SAK

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SUMMARY      #length 349  #molecular-weight 40340  #checksum 5411
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	Query Match	7.3%	Score 559	EB 14	Length 349
Best Local Similarity	27.5%		Pred. No. 5,456	18	
Matches	49	Conserved	49	Nonconserved	60
					Length 9
					Types 7

101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 109

05	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16
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06 112 faplytbaet | b0b0b0b0nkievdaawp 144
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09 127 05p14vfevfevfevfevfevfevfevfevfev 159

```

Search completed: Wed Nov 17 11:02:28 1997
Job time : 43 secs.

14

[illegible][illegible][illegible][illegible]

[illegible]

RESULT	4
ENTRY	JCZ555
TITLE	#type complete
ORGANISM	omec-3 fatty acid desaturase (1994)
DATE	#formal name Nicotiana glauca common tobacco
	14 May 1995 seq-4-1400 version 14 May 1995 final map
	14-May-1995
ACCESSIONS	JCZ555
REFERENCE	JCZ555
authors	Hamada, T.; Kodama, H.; Nishimura, M.; Ibay, K.
journal	Gene (1994) 147:293-294
#title	Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.

```
##status preliminary
##residues 1-319 ##label HAM
##cross-references DDBJ:J26580
##length 319 ##molecular weight 44230 ##formula C1940
```

Only Match 22.6%; Score 110, DR 14, Length 279;
Best Local Similarity 36.43; Pred. No. 1, 160-106;
Matches 125; Conservative 96; Indels 67; Gaps 14.

[illegible]

Dd		137	hgfhgigvetdeswpm--pe-klynk- gys-tklilykpiplilaymylnrkspks	190
Oy		145	HSNCTGLEDVYFTFEETZEMWCEIEHNGTFFWTGTTLTWLITAFNCSHFY	202
Dd		191	-gs--klfpssdlqqlqr-k-yvcslllwmamallsllysalsgmhyfshyl	264
Oy		204	LGGSGHHNPAPINDPEKQIQLISALIAVLLELRFAADANAMVFIVILGL	281

[illegible]

ENTRY	RESULT
552650	5
desaturase delta 15	
formal name Synchocystis sp. (strain P-7803)	
formal name Synchocystis sp.	
formal name Synchocystis sp.	

DATE	28-OCT-1996
ACTIONS	28-OCT-1996
REFERENCE	S52649

#J	Journal	Environ Monit Assess
#Title	Cloning of omega-3 desaturase from <i>Glydinus</i> and its use in altering the degree of methyl group unsaturation.	
#Accession	S52650	
#Status	Preliminary	
#Residues	I-359 #Label SAK	

SUMMARY #cross-references GR.D13780
#length 359 #molecular-weight 41919 #checksum 91627

607,000 2,076,695, 10,000th 3597,
 Best Local Similarity 36.68 Pred. No. 1,990-103;
 877, 1,000th 73; Caps 183;

[illegible][illegible][illegible]

RESULT	6
ENTRY	NQ239
TITLE	# type complete
ORGANISM	omega-3 fatty acid desaturase (EC 1.14.14.-) GMD - soybean
DATE	Shimada, Yam., Oiyama, Tanaka, Shimizu, Nakamura, Soybean
	28 Sep 1993; Experiment performed on Aug 1993; first change
	71-Mar-1996

ACCESSIONS
 002339
 002335
 REFERENCES
 #authors
 Ydary, N.S.; Weizbach, A.; Aeppler, M.; Gaster, C.S.;
 Tschopp, L.; Krensky, A.T.; Bitt, M.E.; Roth, J.L.; J.R.;
 Schwabig, H.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
 Peirer, P.S.; Carlson, T.T.; Russell, S.H.; Fuldman, K.A.;
 Pierce, J.J.; Browne, J.
 Plant Physiol (1994) 103:467-476
 #journal

```

#accession JQ2339
#molecule_type mRNA
#transcript 1-453 ##label YAD
#features features (GB:1.27965

```


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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

```
Run on:      Wed Dec 17 11:11:11 1997,  MasPar time 14.13 Seconds
              794 943 Milliseconds  3.117444e+007
```

Tabular output not generated.

Title:	Accession Number:
1975-08-17-0076	1975-08-17-0076
(1-384) 1975-08-17-0076	1975-08-17-0076

Summary:

Scrolling table:

[illegible]

Post-processing: Minimum Match 0%

Database:

```
1:unann1 2:unann2 3:unann3 4:unann4 5:unannn1 6:unannn2 7:unannn3
8:unannn4 9:unannn5 10:unannn6 11:unannn7 12:unannn8
13:unannn9 14:unannn10 15:unnnrev 16:unnnrev
```

Statistics: Mean 46.871; Variance 102.063; scale 0.455

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	PR	ID	Description	Prod. No.
1	792	25.2	377	5	002477	omega-3 fatty acid	4,360-117
2	787	25.0	385	5	042255	omega-3 fatty acid	6,720-117
3	770	25.4	283	5	A44227	omega-3 fatty acid	6,720-117
4	727	24.0	379	16	JF2958	omega-3 fatty acid	6,666-107
5	705	23.5	453	3	002339	omega-3 fatty acid	7,188-107
6	706	23.1	404	4	020812	omega-3 fatty acid	6,040-107
7	659	23.0	380	5	002336	omega-3 fatty acid	5,038-107
8	697	23.0	446	5	002336	omega-3 fatty acid	2,176-107
9	690	22.8	459	14	052400	acetylcholine	4,726-107
10	267	6.6	317	16	043771	delta-12 desaturase	7,026-23
11	261	8.6	350	16	043772	delta-12 desaturase	6,818-23
12	245	8.1	447	16	052339	n-6 fatty acid desat	2,766-21

Dec 17 11:12 /home/fuller/lec97/US-08-572-027A-8.rpt

13	234	7.9	55.9	56429	beta(1)-caseinase (2.36e+01
14	227	7.5	54932	56432	n-6 fatty acid desat	2.36e+01
15	232	7.5	34916	563770	Delta-12 desaturase	2.14e+18
16	210	6.9	3519	515594	stearoyl-CoA desatur	1.02e+15
17	124	4.2	688	564806	1,49e-03 beta-oxid	1.49e-03
18	107	3.5	35915	855157	beta(4) desaturase	3.36e+01
19	103	3.4	33812	564661	trans-4-enoyl-CoA	2.79e+01
20	102	3.4	55511	564661	trans-4-enoyl-CoA	2.79e+01
21	103	3.4	32716	564442	hydroxyacyl-CoA de	3.72e+01
22	99	3.2	2310	564442	hydroxyacyl-CoA de	2.78e+01
23	100	3.2	234	14039	seroyl protein - 11	2.14e+01
24	100	3.2	236	14039	seroyl protein - 11	2.14e+01
25	100	3.2	236	14039	seroyl protein - 11	2.14e+01
26	100	3.3	43715	564444	seroyl protein - 11	2.14e+01
27	101	3.2	792	563770	seroyl protein - 11	1.55e+01
28	98	3.2	13914	133294	seroyl protein - 11	3.58e+01
29	98	3.2	34514	564444	seroyl protein - 11	3.58e+01
30	98	3.2	38814	565527	oxylactin receptor -	3.58e+01
31	98	3.2	46914	564444	oxylactin receptor -	3.58e+01
32	98	3.2	41914	564522	alpha-galactosidase	3.58e+01
33	98	3.2	45411	561990	hypothetical protein	3.58e+01
34	96	2.2	48514	701987	hypothetical protein	5.95e+01
35	98	3.2	5321	564662	RNA-directed RNA pol	3.58e+01
36	96	3.2	233616	564586	omega-oxoaloxin-sens	5.95e+01
37	96	3.1	7710	564586	hypothetical R, R, p	7.9e+01
38	96	3.1	72214	564745	seroyl protein - 11	7.64e+01
39	96	3.1	13814	559601	seroyl protein - 11	7.64e+01
40	96	3.1	13814	559601	seroyl protein - 11	7.64e+01
41	91	3.0	295	564444	seroyl protein - 11	7.64e+01
42	92	3.0	479	5644210	seroyl protein - 11	7.64e+01
43	91	3.0	49817	5644210	seroyl protein - 11	7.64e+01
44	91	3.0	49817	5644210	seroyl protein - 11	7.64e+01
45	92	3.0	96511	564586	seroyl protein - 11	7.64e+01

ALIGNMENTS

ENTRY	RESULT	1
TITLE	JQ2337	#type complete
ORGANISM	omega-3 fatty acid desaturase (F0114.00.) RN3 - tape	
DATE	30-Sep-1993	#normal homo trisomic fetus #common name tape
REFERENCE	21-Mar-1996	36-Sep-1993 #sequence revision to Aug 1991 #event change
ACCESSION	JQ2337	
REFERENCE	JQ2335	
Author	Yasuy, N.G., Watanabe, N., Asagiri, M., Carter, C.S.	

Journal
Title
plant Physiol. (1993) 103:467-476
Cloning of higher plant omega 3 fatty acid desaturases.

```
##residues      1-377 ##label YAD
##cross-references GB:L33962
```

This enzyme activates the third double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.

CLASSIFICATION: Insect, family, species, fatty acid, carbohydrate
KEYWORDS: cat, cat, database
SYNOPSIS: Length: 300 Km. Weight: 4000g. # of chromosomes: 22, 40

```

Query Match      26.28% Score 7927 DB 57 Length 377;
Best Local Similarity 33.43; E-Val: 1e-4, 3e-119;
Matches 135; Conservative 76; Mismatches 106; Indels 24; Gaps 18;

Dv 2 vvaadqgsaaagddtfdgaagfkiqlrtafrkhwkspldssmsyvarditavala 61
   | : ||| : | | | | | | | | | | | | | | | | | | | | | | | | |
QY 9 VGRPKCKETCHIRKY PCEHTITVSLDAVAIFHEHRCGLPFRFYLLWDTIACCTY 67
   || : ||| : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 vaayt- ds-wlt wpylwaggltwlwtivldhdogagscdpllnatgahll 114
   || : || : | | | | | | | | | | | | | | | | | | | | | | | | |
QY 68 IVALTTHPLRFLFRLFAAEILHWAGVGVHLAWLWLVGKCHHAAEELWMLRTVLHH 127
   ||||| : || : ||| : | | | | | | | | | | | | | | | | | | | | |
Db 115 stlvvygwawshrtthgnqhgvendewypl -pe-ky-knlst-tmltyvpilp 169
   ||||| : || : ||| : | | | | | | | | | | | | | | | | | | | | |
QY 128 SFLVLPYSWMYSHRHNNSTGFEDREVVPRKKSDIKMYCNILNPDLTMTLVAT 187
   || : ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 170 mlayplywyrspk -eg-s hyngysltlusecktl-atstcwsimatlavlst 223
   || : ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 188 -LMPLEPLAFNVWSGMDYGSAWHHRHNPANRYNERHLYTSIDAGLAVCYGLPYRAA- 245
   || : ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 224 lavgptkvgyvpyyltfmwladvrylhnhbdsklpwyrkewslrgltitdtdyg 283
   || : ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 246 WYNAAMWEEGVPELLTWAGLEVLTICLN DPGS-LPAVSSFWFMIGALATATGTCG 303
   || : ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 284 fhmthhdi qthvhhlfprqphlylcyakkuhvlpyrrz 325
   || : ||| : | | | | | | | | | | | | | | | | | | | | | | | | |
QY 304 LHKVFHNTPGTVAHMFTEWGHGHHMAYTVTFITWVC 346
   || : ||| : | | | | | | | | | | | | | | | | | | | | | | | | |

RECORD 2
ENTRY JQ2335 #type complete
TITLE omega-3 fatty acid desaturase (bc_114_99.-) CDS -
ORGNISM #Jornal_name Arabidopsis thaliana #common_name mouse-ear
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #ext_change
ADDITIONS JQ2335
REFERENCE JQ2335
AUTHORS Yadav, N.S.; Wierzbicki, A.; Aegeleer, M.; Oester, C.S.;
Peter, Gary, L.; Kinney, A.J.; Hitz, M.D.; Booth, Jr., J.B.;
Schmeigel, B.; Stecca, R.L.; Allen, J.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.C.; Russell, S.H.; Faldutman, R.A.;
Plencer, J.; Brower, G.
#journal Plant Physiol. (1993) 113:477-476
#title Cloning of hignor plant omega-3 fatty acid desaturases.
#accession JQ2335
##molecule type mRNA
##residues 1-386 ##label YAD
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.
CLASSIFICATION Superfamily omega 3 fatty acid desaturase
category oxidoreductase
KATHOBS
SUMMARY #length 386 #molecular_weight 44076 #characem R044

Query Match 26.0%; Score 7477 DB 57 Length 386;
Best Local Similarity 39.1%; E-Val: 1e-4, 5e-118;
Matches 137; Conservative 74; Mismatches 111; Indels 24; Gaps 18;

Dv 8 ltumdgpyatknkwetldfgaagfkiglrtafrkhwkspldssmsyvrditlava 67
   | : ||| : | | | | | | | | | | | | | | | | | | | | | | | | |
QY 6 RMQVSPPSKAKETNNIKRP-PENRRPFYVGELAKRIAPRRKRSPRSYSLTWIOTIIAS 64

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[illegible]

姓名: _____
 学号: _____
 班级: _____
 日期: _____

Research and Development Department, for Research Unit
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MP-100 gp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 17 11:00:41 1997, MaxParTime 10.08 Seconds

Tabular output not generated.

Title: *See the 5700A*
Description: (1 384) *See 5700A 2007b, p. 2009*

$$V_{\text{eff}} = \frac{1}{2} \left(\frac{1}{\mu} + \frac{1}{\mu_0} \right) \left(\frac{1}{\mu} + \frac{1}{\mu_0} \right) \left(\frac{1}{\mu} + \frac{1}{\mu_0} \right)$$

Scoring table: PAM 150

Searched: 59021 Sept, 2010 00:00:00

Post-processing: Minimum Match 0%

Database: swiss-prot34

8:part8 9:part9 10:part10 11:part11

Statistics: Mean 48.387; Variance 84.464; Std. Dev. 9.1899

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summary

Result No.	Score	Query Match	Length	OR	ID	Description	Prod. No
1	2116	89.9	383	3	ED3E_APAAR	OMEGA-6 FATTY ACID DE	0.000-0.000
2	2217	76.7	283	2	ED3E_GGAAA	OMEGA-6 FATTY ACID DE	0.000-0.000
3	2217	76.7	283	2	ED3E_GGAAA	OMEGA-6 FATTY ACID DE	0.000-0.000
4	777	75.7	317	3	ED3E_BHAAA	OMEGA-3 FATTY ACID DE	4.140-1.140
5	769	75.4	386	3	ED3E_APAAR	FATTY ACID DE	0.000-0.000
6	754	75.0	383	3	ED3E_BPAAR	FATTY ACID DE	0.000-1.140
7	725	74.0	380	3	ED3E_PPAAR	OMEGA-3 FATTY ACID DE	5.650-1.140
8	717	73.7	374	3	ED3E_PPAAR	FATTY ACID DE	4.110-1.140
9	711	73.5	490	3	ED3E_PPAAR	OMEGA-3 FATTY ACID DE	1.000-1.140
10	685	72.7	422	3	ED3E_PPAAR	FATTY ACID DE	0.000-1.140
11	682	72.6	474	4	ED3E_GGAAA	OMEGA-6 FATTY ACID DE	0.000-0.000
12	681	72.5	320	3	ED3E_GGAAA	OMEGA-6 FATTY ACID DE	0.000-1.140
13	678	72.4	474	4	ED3E_APAAR	FATTY ACID DE	4.140-1.140

14	665	22.6	447	3	FD3D	PELIN	OMEGA-3 FATTY ACID DE	4.78e-118
15	655	21.7	435	3	FD3D	ARATH	TEMPERATURE SENSITIVE	9.98e-118
16	735	8.4	447	3	FD3D	SPILOT	OMEGA-6 FATTY ACID DE	4.15e-72
17	703	6.3	443	3	FD3D	COYPOK	OMEGA-6 FATTY ACID DE	7.78e-78
18	751	8.3	443	3	FD3D	BPANA	OMEGA-6 FATTY ACID DE	2.70e-72
19	722	7.3	418	3	FD3D	APAHN	OMEGA-6 FATTY ACID DE	1.77e-72
20	711	7.4	343	3	FD3D	COYCI	FATTY ACID SENSITIVE	5.44e-70
21	708	3.2	386	7	QYVY	FIC	OXIDATION RESISTANCE (OT	5.81e-21
22	98	2.2	350	7	QYVY	HOHMT	OXIDATION RESISTANCE (OT	6.91e-21
23	96	3.2	419	1	AAAL	MEGEE	ALPHA-OXALATE DEHYDRA	1.07e-60
24	96	3.2	515	9	SMET	YEAST	TRANSPORTER PROTEIN S	1.07e-60
25	96	3.2	975	2	CLIN	YEAST	C-1-TETRAHYDROBOLATE	1.07e-60
26	94	3.1	275	1	AMSA	NITRO	AMMONIA MONOXYGENASE	1.92e-60
27	94	3.1	428	1	WIAL	CHITD	VITAMIN C-1 DEHYDROGE	1.92e-60
28	93	3.1	429	9	QYVY	AAAL	HYDROLYTIC DEGRADATION	1.92e-60
29	94	3.1	189	4	QYVY	FAT	INTERFERON MEMBRANE CH	1.92e-60
30	96	2.8	205	8	HAAR	FAH1	HAS RELATIVE GLOBULIN B	6.70e-50
31	91	3.5	419	4	QYVY	HOHMT	ALPHA-OXALATE DEHYDRA	4.71e-60
32	91	3.9	773	1	QYVY	MEGEE	ALPHA-OXALATE DEHYDRA	4.71e-60
33	91	3.0	413	1	H2AH	HUMAN	H2A-2 ADRENOCORTIC HED	4.71e-60
34	90	3.0	410	1	QYVY	MEGEE	ADRENOCORTIC HED	4.29e-60
35	92	3.0	423	4	QYVY	CHITD	HYDROLYTIC DEGRADATION	3.52e-60
36	92	3.0	417	10	QYVY	MEGEE	HYDROLYTIC DEGRADATION	3.52e-60
37	91	3.2	515	1	AAAL	MEGEE	ALPHA-OXALATE DEHYDRA	4.71e-60
38	90	3.6	425	11	QYVY	MEGEE	ALPHA-OXALATE DEHYDRA	4.71e-60
39	91	3.1	400	1	QYVY	MEGEE	ALPHA-OXALATE DEHYDRA	4.71e-60
40	91	3.1	433	4	QYVY	MEGEE	ALPHA-OXALATE DEHYDRA	4.71e-60
41	91	3.0	693	9	TGLS	MOOSE	PROTEIN-GLUTAMINE GLO	4.71e-60
42	90	2.0	702	19	QYVY	CSVI	HYDROLYTIC DEGRADATION	6.29e-60
43	92	3.0	189	4	QYVY	FAH1	HAS RELATIVE GLOBULIN B	6.70e-50
44	41	3.0	211	2	CLIN	BARIT	DICHLOROPYRIMIDINE SINS	4.71e-60
45	42	3.2	189	4	QYVY	FAH1	HAS RELATIVE GLOBULIN B	6.70e-50

ALIGNMENTS

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01 RESULT 1
02
03 ID EEAR_ABRACH CCMARWARD; PRT; 183 AA.
04 AC P46513;
05 DT 01-NOV-1995 (REEL 32, CREATED)
06 DT 01 NOV 1995 (APRIL 32, LAST SEQUENCE UPDATE)
07 DT 01-FEB-1996 (REEL 33, LAST ANNOTATION UPDATE)
08 DE OMEGA-6 FATTY ACID DEHYDROGENASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
09 DE (OLETA 12 DECATERASE).
10 FM2.
11 ARABIDOPSIS THALIANA (MOORE-EAR CRESS).
12 CC ENZYMOLOGY, FLAVIN, ENZYME ACTIVITY, ANGIOTENSINASE, DISULFIDEISOMERASE,
13 CAPPAVALLES; CRUCIFERAE.
14 RN 11)
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16 FM SEQUENCE FROM N.A.
17 FM SKUFFY J., LIECHTEN J., FRIEDMAN K., YANIV N., LANE E., BRADSHAW J.;
18 FM MEDLINE; 94176997.
19 FM PLANT CELL 6:147-158(1994).
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OC PARACAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SEED;
 RA MADON, 94302147.
 RA YAO, N.S., WIERZBICKI A., AGERENTER M., CASTER C.S., PEREZ-GRAN L.,
 RA KINNEY A.J., HITE M.D., BOOTH J.R. JR., SCHMEITZER R., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., ARLESON T.J., RUSSELL S.H.,
 RA FELDMANN K.A., PIERCE J., BROWSE J.;
 RA PLANT PHYSIOL. 103:467-476(1993).
 RU
 CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE HOPEBONDS OF 14:3 AND 18:3 FATTY
 CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALA-OLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE BOUND (PROBABLY)
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAIN MAY CONTAIN THE ACTIVE SITE
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA 3 FATTY ACID DESATURASES.
 DR EMBL, L22963; G4061947.
 DR PIR, J02339; J02339.
 KM OXIDOREDUCTASE, FATTY ACID DESATURATING, CHLOROPLAST, MEMBRANE,
 KM TRANSIT PEPTIDE.
 FT TRANSIT 1 ?
 FT CHAIN 1 446
 FT DOMAIN 171 175 HISTIDINE BOX 1.
 FT DOMAIN 207 211 HISTIDINE BOX 2.
 FT DOMAIN 374 378 HISTIDINE BOX 3.
 FT SEQUENCE 453 AA; 51352 MW; 54314.25 CSQ33;
 SQ
 Query Match 22.4% Score 687, FR 3, Length 453;
 Best Local Similarity 38.53% Ident. No. 110, 124;
 Matches 126; Conservative 45; Mismatches 104; Indels 77; Gaps 18;
 Db 98 p9appgffadlaaalkphwkwkfpmsyvvdiv--w-qlaaaay--l-n nsl 150
 Y 25 FQSEFFIVQELKRAHREHRCNRCG--LWLLACQYXATYTHLHFLST 84
 Db 151 wvplyaaqgfmalfvlgndqghsfnskslnsvghllhselivphvghwlsrth 210
 Y 65 AMPLWAOQ-VLTGVWVAHRCCHAHSHDVMLDVGLFHSGLIVEFESMKSHRH 144
 Db 211 kghhgaedswphl--pe klf rslde vtmeltfapflstfpyl fscs pg 262
 Y 145 HSNGLSLEDEVFPRKEDUKWCKRTLSLCKTWTETVCTE CMFLALFNVSQRF 203
 Db 263 kty--shfsssdlypnerkv--itsacwaamglvqlyfmgpdlkllypvyv 319
 Y 294 DSGEHLRHKHALTYSGHLALYISNAQYLVVYVTP VAAVNAWV-T-VVHLI 262
 Db 320 lvmjdlvlylhhghcklpyrghkewylygltlddygwinmihdd-qthvhh 378
 Y 263 VNGEVLVLTIGH-THPS-LPHYDSSKMGFGALAVDRDGLINKVHNITDTHAHH 320
 Db 379 lfqfphylveateakpvdikyr 404
 Y 321 PFTMPHAEATKALPDLGEYQ 346
 RESULT 11
 ID FD3C GRANA STANDARD; PRT; 404 AA.
 AC P48618;

DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-)
 DE (FRAGMENT).
 ON FAD7.
 OS BRASSICA NAPUS (RAPE).
 AC FRERADY, FANTY, ENYDRETTA, ANTOCOPMAD, DTCVYVYDEAE;
 OC CAPPALES, CROCIPEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SEED;
 RA MADON, 94302147.
 RA YAO, N.S., WIERZBICKI A., AGERENTER M., CASTER C.S., PEREZ-GRAN L.,
 RA KINNEY A.J., HITE M.D., BOOTH J.R. JR., SCHMEITZER R., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., ARLESON T.J., RUSSELL S.H.,
 RA FELDMANN K.A., PIERCE J., BROWSE J.;
 RA PLANT PHYSIOL. 103:467-476(1993).
 RU
 CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE HOPEBONDS OF 14:3 AND 18:3 FATTY
 CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALA-OLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE BOUND (PROBABLY)
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAIN MAY CONTAIN THE ACTIVE SITE
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA 3 FATTY ACID DESATURASES.
 DR EMBL, L22963; G4061947.
 DR PIR, J02339; J02339.
 KM OXIDOREDUCTASE, FATTY ACID DESATURATING, CHLOROPLAST, MEMBRANE,
 KM TRANSIT PEPTIDE.
 FT TRANSIT 1 1
 FT CHAIN 1 404
 FT DOMAIN 121 125 HISTIDINE BOX 1.
 FT DOMAIN 157 161 HISTIDINE BOX 2.
 FT DOMAIN 324 328 HISTIDINE BOX 3.
 FT SEQUENCE 404 AA; 46617 MW; 767199 CSQ32;
 SQ
 Query Match 22.4% Score 627, DB 3, Length 404;
 Best Local Similarity 37.13% Ident. No. 5, 536 124;
 Matches 126; Conservative 81; Mismatches 112; Indels 21; Gaps 14;
 Db 33 sspieepklyfdpypptladiiaalkphwkwkfpmsyvvdiv--lala 90
 Y 10 SHCKKGLDFIKKNCULHITVQELKALPHRCSCIFRSSTL--LHIAQFYV 59
 Db 91 agday--l-r--nwlpwlyaaqgfmalfvlgndqghsfnskslnsvghllhs 145
 Y 70 ATTYPLPHNLSTYAWLWAOQSVLTGVWVAHRCCHAHSHDVMLDVGLFHSF 129
 Db 146 jlypvywlshtthghghvndeswhpm--se-ky-ksldkp-ttfrtlblvml 200
 Y 130 LAVEFYSKTYHPSCHNITGSLREVFVPRFTDLYWYGTLDNPTDNYMIVQFT-L 188
 Db 201 aygfylwaispgk--kgs--hyhpsddflpkerndvltacawamavllvclfyng 255
 Y 109 GWPLDGFNVSKRF DGGK KCHHNAFTHDREKQGLTSSGAAZVYVDFRFAQDC 248
 Db 256 pmqnlklyvpywvwnmldivlylhhghcklpyrghkewylygltlddygwin 315
 Y 249 VASWVGYGVPLLVNGEVLVLTIGH-THPS-LPHYDSSKMGFGALAVDRDGLINK 306

Dec 17 11:04

home/filler/dec97/US-08-572-027A-4.np

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DR EMBL, L66296; G438451; -
 KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KM TRANSMEMBRANE
 FT TRANSMEM 56 76 POTENTIAL
 FT TRANSMEM 117 137 POTENTIAL
 FT TRANSMEM 179 199 POTENTIAL
 FT TRANSMEM 225 245 POTENTIAL
 FT TRANSMEM 292 272 POTENTIAL
 FT DOMAIN 105 109 HISTIDINE BOX 1
 FT DOMAIN 141 145 HISTIDINE BOX 2
 FT DOMAIN 315 319 HISTIDINE BOX 3
 SQ SEQUENCE 383 AA; 4404 / MW; 19203435 CRO322

Query Match 89.4%; Score 2704; DB 3; Length 383
 Best Local Similarity 88.5%; Pred. No. 0.00e+00;
 Matches 340; Conservative 23; Mismatches 20; Indels 1; Gaps 1;

Db 1 mgagimprptskksetcttkvpcskpfsvydlkaiqphcfrksifrsfyslisd 60
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 QY 1 MGAGIMPRPTSKKSETCTTKVPCSKPFVSYDLKAIQPHCFRKSIFRSFYSLISD 60

Db 61 llsacfyvavnyfsliprpisylawpilywacqcyvlgwajhocphafasywld 120
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 QY 61 LLSACFYVAVNYFSLIPRPISYLAWPILYWACQCYVLGWAJHOCPHAFASYWLD 120

Db 121 twglilhsallvpylsmsyhtlmsatgslvclvfpkysakkykylmnpilam 180
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 121 TWGLILHSALLVPLYLSMSYHTLMSATGSLVCLVFPKYSAKKYLKNPILAM 180

Db 181 mlvqftlqmplylawnvsgnyfcdofrcghhnmilthbhracqylldacilavtcl 240
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 181 MLVQFTLQMPLYLAWNVSQNYFCDOFRCHHNMILTHBHRACQYLLDACILAVTCL 240

Db 240 yryaaagmasmscllyrpfllwratvlllylshfslphysaswmlgjalvdr 299
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 240 YRYAAAGMASMSCLLYRPFLLWRATVLLLYLSHFSLPHYSASWMLGJALVDR 299

Db 300 dyglnkvlnludlthvahlstcmphymacckaklilpdyfjgfywamyrea 359
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 300 DYGLNKVFNILUDLTHVAHLSTCMPHYMACCKAKLILPDYFJGFYWAMYREA 359

Db 360 keciyvepdqgskkyvwnkl 383
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 360 KECIYVEPDQGSKKYVWNKL 383

RESULT 2
 ID FDB6 SOYBN STANDARD; PRT; 383 AA.
 AC P48631;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 2
 DE (EC 1.14.99.-).
 GN PAD2-2.
 OS GLYCINE MAX (SOYBEAN).
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
 OC FABACEAE.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=EPICOTYL;
 RX MEDLINE: 96151506.
 RA HEPBARD E.P., KINNEY A.J., STECCA K.L., Miao G.H.;
 PL PLANT PHYSIOL. 110:311-319(1996).

Dec 17 11:04

home/filler/dec97/US-08-572-027A-4.np

4

CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE DOUBLE BOND IN THE BIOSYNTHESIS OF SAT FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
 DR EMBL, L43921; G504154; -
 KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KM TRANSMEMBRANE
 FT TRANSMEM 61 81 POTENTIAL
 FT TRANSMEM 85 105 POTENTIAL
 FT TRANSMEM 117 137 POTENTIAL
 FT TRANSMEM 179 199 POTENTIAL
 FT TRANSMEM 225 245 POTENTIAL
 FT TRANSMEM 249 269 POTENTIAL
 FT DOMAIN 105 109 HISTIDINE BOX 1
 FT DOMAIN 141 145 HISTIDINE BOX 2
 FT DOMAIN 315 319 HISTIDINE BOX 3
 SQ SEQUENCE 383 AA; 41467 MW; 1465721 CRO322

Query Match 76.2%; Score 2305; DB 3; Length 383
 Best Local Similarity 77.1%; Pred. No. 0.00e+00;
 Matches 296; Conservative 41; Mismatches 46; Indels 1; Gaps 1;

Db 1 mgagimprptskksetcttkvpcskpfsvydlkaiqphcfrksifrsfyslisd 60
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 1 MGAGIMPRPTSKKSETCTTKVPCSKPFVSYDLKAIQPHCFRKSIFRSFYSLISD 60

Db 61 llsacfyvavnyfsliprpisylawpilywacqcyvlgwajhocphafasywld 120
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 61 LLSACFYVAVNYFSLIPRPISYLAWPILYWACQCYVLGWAJHOCPHAFASYWLD 120

Db 121 twglilhsallvpylsmsyhtlmsatgslvclvfpkysakkykylmnpilam 180
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 121 TWGLILHSALLVPLYLSMSYHTLMSATGSLVCLVFPKYSAKKYLKNPILAM 180

Db 181 mlvqftlqmplylawnvsgnyfcdofrcghhnmilthbhracqylldacilavtcl 240
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 181 MLVQFTLQMPLYLAWNVSQNYFCDOFRCHHNMILTHBHRACQYLLDACILAVTCL 240

Db 240 yryaaagmasmscllyrpfllwratvlllylshfslphysaswmlgjalvdr 299
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 240 YRYAAAGMASMSCLLYRPFLLWRATVLLLYLSHFSLPHYSASWMLGJALVDR 299

Db 300 dyglnkvlnludlthvahlstcmphymacckaklilpdyfjgfywamyrea 359
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 300 DYGLNKVFNILUDLTHVAHLSTCMPHYMACCKAKLILPDYFJGFYWAMYREA 359

Db 360 keciyvepdqgskkyvwnkl 383
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 360 KECIYVEPDQGSKKYVWNKL 383

RESULT 3
 ID FDB6 SOYBN STANDARD; PRT; 387 AA.
 AC P48630;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

[illegible]

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FT TRANSMEM 62 83 POTENTIAL.
FT TRANSMEM 226 240 POTENTIAL.
FT TRANSMEM 212 262 POTENTIAL.
FT DOMAIN 101 105 HISTIDINE BOX 1.
FT DOMAIN 112 141 HISTIDINE BOX 2.
FT DOMAIN 304 308 HISTIDINE BOX 3.
FT DOMAIN 346 447 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1
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CC AND/OR BE INVOLVED IN METAL ION BINDING.
OC -L- SIMILARITY TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
DB EMBL J01416; G16149; .
KW OXIDOREDUCTASE; FATTY ACID MONOOXYGENASE; ENDOPLASMIC RETIUMNG;
NM TRANSMEMBRANE.
FT TRANSMEM 53 73 POTENTIAL.
FT TRANSMEM 210 230 POTENTIAL.
FT TRANKMEM 224 274 POTENTIAL.
FT DOMAIN 98 102 HISTIDINE BOX 1.
FT DOMAIN 134 138 HISTIDINE BOX 2.
FT DOMAIN 301 305 HISTIDINE BOX 3.
QV EVIDENCE 363 AA, 4336 MW, 536ADDS OF 102.

Query Match      25-65; Score 716; DB 3; Length 385;
Best local Similarity 41.0%; Field No. 2,71e+144;
Matches 134; Conserved 69; Mismatches 29; Indels 25; Gaps 13;

Db    25 psapbfklydraralphnkwvksplmsyvtldlavala madyf---d--swf 77
     | ||| :||| :||| :||| ||| :||| ||| :||| :||| :||| :|||
QY    25 FEETRETVELKLLHHLHRLRDLRYEYLGLTTLTAAT YGVVAATTELTGRTTR 24
Db    78 lwpilyvaagtlfwatylqhdgfsfdiplnsvrhlhsflipybhwtiruth 137
     ||||| ||| :||| :||| :||| ||| :||| ||| :||| :||| :|||
QY    85 AMPLYMAQQCVCLTWAVIAHQGHASSDVMUDVTALLFHSFLDIOTFSMTYSRRH 144
Db    138 hahghdvndewypf pe kty knlfnss rtmryvdplmpaypylwyspqk-- 190
     ||| ||| ||| ||| :||| ||| :||| ||| :||| :||| :||| :|||
QY    145 ISNNTSLSEDEVYVCTDSTCRKLNDRCHQLMLVCEI LMPITLENVSDEGT 203
Db    191 ew--s--htppslagswklratstowimlael --ylvslidovvlkv yrrpy 245
     ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY    234 DGGFRCHFRAFIINMDELWISDA GLAAV NRIIRANVGWSMVCTTFVEED 261
Db    246 ltymiladvlyhhqdcklpmygskewslylglttiddygntnnhda-gtvnh 304
     + + :||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY    252 FNCTDLVLTYQH THRS HNRSTSWCMZCATAYVDGDTLDLPENAHHRHVRV 319
Db    335 hlfpdlphlvdatlrakhlvlyyr 331
     ||| :||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY    320 HLESTMHYAMEATRKAIRKLGEYQ 346

RESULT   7
ID       7D3E PHAMU STAFFARY PRY 360 AA.
AC P32291).
DT 01-OCT-1993 (REL 27, CREATED)
DT 01-OCT-1993 (REL 27, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL 33, FAST ANNOTATION UPDATE)
DEF OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETIUMNG (P01349.-)
CA (INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1).
CS ARGI.
OS PHASEOLUS AUREUS (MING BEAN) (VIGNA PAULATA).
NC BUKARUYOTA PLANTA; EMBOYOPIITA; ARCHIOSTERMA; DICOTYLEDONEAE; PAPILLAE; FABACEAE.
RC TISSUE=HYPOCOTYL;
RA YAMAMOTO K.T.; MORI H.; IMAGAKI H.;
RD PLANT CELL PHYSIOLO. 33:13-20(1992).
CU -L- FUNCTION: MICROSOFT (MS) OMEGA-3 FATTY ACID DESATURASE INTRODUCES THE THIRD DOUBLE-BOND IN THE RESIDUAL CHAIN OF A C-18 FATTY ACID. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE CYTOCHROME BS AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO PHOSPHATIDYLETHANOL AMINE, PO-SHUB; OTHER
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100 PHOSPHOLIPIDS.
 99 1. FATTY ACID HYDROXYLATION; FATTY ACID HYDROXYLATION;
 98 2. SUBCELLULAR LOCATION: PROPOLYSACCHARIDE; PROPOLYSACCHARIDE;
 97 3. NAME: THE HYDROXYLATION BOX COULD BE A SIGNAL FOR THE ACTIVE SITE
 96 AND/OR BE INVOLVED IN METAL ION BINDING.
 95 4. INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
 94 5. SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID HYDROXYLASES
 93 6. NAME: 24:6n-3 HYDROXYLASE.
 92 7. SUBCELLULAR LOCATION: FATTY ACID HYDROXYLATION; ENDOPLASMIC RETICULUM;
 91 8. TRANSMEMBRANE.
 90 9. TRANSMEMBRANE.
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 -126 225. TRANSMEMBRANE.

FT	CHAIN	2	446	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST.
FT				
FT	DOMAIN	163	167	HISTIDINE BOX 1.
FT	DOMAIN	199	203	HISTIDINE BOX 2.
FT	DOMAIN	366	370	HISTIDINE BOX 3.
SEQUENCE		446 AA;	5174 NO.	EMBL/CCD/370250.

Query Match 22.0%; E-value 6.7; 2N 3; Length 446;
 Best Local Similarity 33.1%; Filed No. 6,276-126;
 Matches 127; Conservative 75; Identical 113; Indels 26; Gaps 16.

[illegible]

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RESULT 14
ID FD3C SESIN STANDARD; PRT; 447 AA.
AC P46620;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMGA-3 FATTY ACID TRIESTERASE, TRIESTERASE ESTERASE (EC 3.1.1.41-3.1.1.42).
GN FAL7.
NC CATABOLIC METABOLISM (GENERAL TERMS) (CATABOLISM)
NC EUCALYPTAL; PLANTAL; EUCALYPTALAL; AUCOCOSYMATAL; HYDROXYLIPIDAL;
NC SCOPHODIARIALAL; PEDALINACAL.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. 4294; TISSUE=OVULETEND;
RA SHOU K.;
RL SINGHITTE (APR 1995) TO EMULSIFY TRIESTER FATA SALTS.
RL -1. FUNCTION: CHLOROPLAST OMGA-3 FATTY ACID DEHYDROGEN INTERCONVERT
CC CC THE THIRD DOUBLEDOWN IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERRULOIC AC AS ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC EXHIBITED TO CALICULIFEROL, SULFOGLUCUS AND PHOSPHATIDYLINOSITOL.
CC -1. PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1. SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLY).
CC -1. DOMAIN: THE HISTIDINE BOX DOMAIN MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1. SIMILARITY: TO OTHER PLANT OMGA-3 FATTY ACID DESATURASES.
CC EMUL; 075817; 09/09/94; ..
CC OXIDOREDUCTASE; FATTY ACID HYDROLYSIS; CHLOROPLAST; MEMBRANE-
CC

```

[illegible][illegible]

RESULT	15	STANDARD	FRT	430 AA.
1D	FD3D ARATH			
A7	P48622/			
DT	01-FEB-1996 (REL. 33, CREATED)			
DT	01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)			
DT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)			
DT	SEQUENCE GENERATED BY A LARRY AUST SEQUENCER, PROTIPLAST			
DT	SEQUENCER (REV. 1.14.94.-).			
GN	FAD8.			
05	ARABIDOPSIS THALIANA (MOORE-EAR CRESS).			
06	ERIKABOLA; PLANTA; EMBRYONICITA; ANGIOSPERMAT; Dicotyledoneae;			
07	CAPPALES; PRINIFRAB.			
11				
FN	SEQUENCE FROM N.A.			
FT	SPALM-IV; POLYMERIA; TISSUE-APICAL PARTS;			
FX	MEDLINE# 9106742.			
PA	GERSON S., ARONOFF V., IN: R., SOMEVILLE C./			
PL	PLANT PHYSIOL. 1984;105:1621(1984).			
12				
RN	SEQUENCE FROM N.A.			
RP	SPALM-IV; POLYMERIA; TISSUE-APICAL;			
RT	SEQUENCE FROM N.A.			
RI	SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBD DATA BANKS.			
CI	FUNCTION: CHLOROPLAST GEN-3 PATTY ACIN DEGRADATION			
01	THE LEAFY PROTEIN IN THE PROTEINOMES OF 16-3 AND 18-3 PATTY			
02	A-100, MEMBRANE INTEGRATION OF PLANT MEMBRANE. 15-15 THOUGHT			

39 22 1.9 362 112 AT553429 A. thaliana transcrib 1.49e-04
 40 22 1.9 401 167 1/0663 57 vegetative meriste 7.49e-04
 41 22 1.9 454 145 945/1 y-fk11-1st. Scores for 7.49e-04
 42 22 1.9 411 40 R41655 yfduauyrl homo seple 7.49e-04
 43 22 1.9 444 10 yfduauyrl homo seple 7.49e-04
 44 22 1.9 444 116 W/800K 1 yf12 Human retina ch 7.49e-04
 45 22 1.9 444 117 W/800K 1 yf12 Human retina ch 7.49e-04

ALIGNMENTS

RESULT 1
 LOCUS H36908 608 bp mRNA EST 25 JUL 1995
 DEFINITION 15037 Arabidopsis thaliana cDNA clone 180K1517.
 ACCESSION H36908
 MID 9906407
 KEYWORDS EST.
 SOURCE thale cress clone=180K1517 library=lamba-PRI2 strain=var columbia
 vector=lamba Zip lox primer-T7 dye primer Rstlet Sal Rstlet-Sal
 lambda PRI2 is a cDNA library derived from equal quantities of 4
 pools of mRNA. The cDNA sources were 1) 7 day germinated etiolated
 seedlings; 2) tissue culture grown roots; 3) staged plants half
 with 24 hour light cycle, half on 16 hr light, 8 hour dark
 rosettes; 4) same plants as 3 but aerial tissue (stems, flowers
 and siliques). The vector is BRV's lambda Zip-lox. The cDNA
 inserts were directionally cloned with Sal-Not arms using oligo dT
 primed cDNA.

ORGANISM Arabidopsis thaliana
 Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;
 Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 608)
 AUTHORS Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H.,
 McIntosh, L., Ollivierre, J., Ralke, N., Somerville, C., Thomas, W.M.,
 Reitel, E. and Somerville, C.

TITLE Genes galore: a summary of methods for accessing results from
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 JOURNAL Plant Physiol. 106, 1241-1255 (1994)

COMMENT

Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU-DOE-PRU, Michigan State University, Plant Biology Bldg., E.
 Lansing, MI
 Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 2231stc@idm.ci.msu.edu.

FEATURES
 source location/Qualifiers
 1..608
 /organism="Arabidopsis thaliana"
 /clone="180K1517"
 /strain="var Columbia"
 126 a 158 c 126 g 126 t 20 others

Query Match 27.2%; Score 314; EB 44; Length 608;
 Best Local Similarity 80.7%; Freq. No. 0.000000;
 Matches 432; Conservative 0; Mismatches 98; Indels 5; Gaps 4;

Db 1 catcattatagcctcatgctctctactacgtggccacccaatctctctctctctctca 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 GY 177 CATATATATAGCCTCATGCTCTCTACTACGTGGCCACCAATCTCTCTCTCTCTCA 236
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 Db 61 ggcctctctctacttgggttgggttgggttgggttgggttgggttgggttgggttgg 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

GY 251 cctctctctctctctctctctctctctctctctctctctctctctctctctctct 296
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 121 tggctgggtctggcctggcctggcctggcctggcctggcctggcctggcctggcct 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 GY 294 cctctctctctctctctctctctctctctctctctctctctctctctctctct 356
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 Db 181 tggctgggtctggcctggcctggcctggcctggcctggcctggcctggcctggc 240
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 GY 357 cctctctctctctctctctctctctctctctctctctctctctctctctctct 416
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 Db 241 tggctgggtctggcctggcctggcctggcctggcctggcctggcctggcctggc 300
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 GY 417 cctctctctctctctctctctctctctctctctctctctctctctctctctct 476
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 Db 301 cctctctctctctctctctctctctctctctctctctctctctctctctctct 360
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 GY 477 cctctctctctctctctctctctctctctctctctctctctctctctctctct 536
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Db 361 cctctctctctctctctctctctctctctctctctctctctctctctctctct 420
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 GY 537 cctctctctctctctctctctctctctctctctctctctctctctctctctct 595
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 Db 421 tggctgggtctggcctggcctggcctggcctggcctggcctggcctggcctggc 477
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 GY 546 cctctctctctctctctctctctctctctctctctctctctctctctctctct 604
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 Db 478 cctctctctctctctctctctctctctctctctctctctctctctctctctct 532
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 GY 645 cctctctctctctctctctctctctctctctctctctctctctctctctctct 704

RESULT 2
 LOCUS H36908 512 bp mRNA EST 17 AUG 1995
 DEFINITION 15037 Arabidopsis thaliana cDNA clone 145C277.
 ACCESSION H36908
 MID 9949806
 KEYWORDS EST.

SOURCE

thale cress clone=145C277 library=lamba PRI2 strain=var columbia
 vector=lamba Zip-lox primer-T7 dye primer Rstlet-Sal Rstlet-Sal
 lambda PRI2 is a cDNA library derived from equal quantities of 4
 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated
 seedlings; 2) tissue culture grown roots; 3) staged plants half
 with 24 hour light cycle, half on 16 hr light, 8 hour dark
 rosettes; 4) same plants as 3 but aerial tissue (stems, flowers
 and siliques). The vector is BRV's lambda Zip-lox. The cDNA
 inserts were directionally cloned with Sal-Not arms using oligo dT
 primed cDNA.

ORGANISM Arabidopsis thaliana
 Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;
 Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 512)
 AUTHORS Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H.,
 McIntosh, L., Ollivierre, J., Ralke, N., Somerville, C., Thomas, W.M.,
 Reitel, E. and Somerville, C.

TITLE Genes galore: a summary of methods for accessing results from
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 JOURNAL Plant Physiol. 106, 1241-1255 (1994)

COMMENT

Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU-DOE-PRU, Michigan State University, Plant Biology Bldg., E.
 Lansing, MI
 Tel: 517-353-0854

[illegible]

RESULT	8				
LOCUS	M43526	534 bp	EMBL	EST	21 MAY 1996
DEFINITION	22993-10414 Arabidopsis thaliana cDNA clone library.				
ACCESSION	M43526				
NID	91327994				
KEYWORDS	EST.				
SOURCE	thale cress.				
ORGANISM	Arabidopsis thaliana				
	Eukaryote; mitochondrial; eukaryote; Viridiplantae;				
	Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;				
	Magnoliopsida/Capparales; Brassicaceae/ Arabidopsis.				
REFERENCE	1 (bases 1 to 534)				
AUTHORS	Newman,T., deBorja,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,B., Ollivier,M., Rabin,N., Somerville,C., Reitel,E. and Somerville,C.				
TITLE	Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones				
JOURNAL	Plant Physiol. 106, 1241-1253 (1994)				
MEDLINE	95148729				
COMMENT					

CONTACT: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU-DOE-PR, Michigan State University, Plant Biology Bldg., E.
 Lansing, MI
 Tel: 517-353-0824
 Fax: 517-353-9168
 Email: 2233lc@msu.edu
 Seq primer: T7.
FEATURES: *Escherichia coli* strains
SOURCE: 1.354

```

/organism="Arabidopsis thaliana"
/strain="Columbia"
/notes="Vector: pBluescript SR, Site 1: EcoRI, Site 2:
EcoRI, Using 5 ug of poly(dA)enylated cDNA from 3 day-old
Arabidopsis thaliana (Columbia) seedling hypocotyl as
template and oligo d(T) as primer, first strand synthesis
was catalyzed by Moloney murine leukemia virus reverse
transcriptase (Pharmacia). Second strand cDNA was made
using the procedure of Gelbart and Millman (1983) except
that DNA ligase was omitted. After the second strand

```

fragment, the ends of the cDNA were made blunt with Klenow fragment and EcoRI/XbaI adaptors (Pharmacia) were ligated to each end. The cDNA was purified from unligated adaptors by spin-column chromatography using Sephadryl s-300 and size-fractionated on a 1% low melting point mini-gel. Size selected cDNAs (3 - 6 kb) were removed from the gel using agarase (New England Biolabs), phenol:chloroform extracted and precipitated using 0.3 M NaAc (pH 7.4)/ethanol. A portion of each cDNA size-fraction (0.1 µg) was co-precipitated with 1 µg of LambdaPhi (Stratagene) digested, phosphorylated arms and then ligated in a volume of 4 µl overnight. Each ligation mix was peak-digested in vitro using *AluI*-XbaI and packaging extract (Stratagene). We have determined that although first strand cDNA synthesis was initiated using dT₁, almost all of the cDNAs begin 8-10 bp from the poly-A tail. The reason for the loss of the poly-A tail is most likely due to lower than anticipated nucleotide levels during the Klenow fill-in of 3'-5' ends before the addition of linkers (3'-5' ends instead of 5'-3' poly-A tail). When this library is used please reference the ABRC and: Kiebert, C. et al. (1993) Cell 76:427-441.

/clone="H1C127"

/clone="Lib-CDA-16"

/tissue type="seeding hypocotyl"

/dev stage="3 day-old"

size="534"

141 a 113 c 145 t 21 others

[illegible]

(a)

Dec 17 17:37

Home/fulle/dec97/US-08-572-027A-7.rst

17

LOCUS 722639 433 bp PCR EST 07 AUG 1996
 DEFINITION 4647 Arabidopsis thaliana cDNA clone J05G017.
 ACCESSION T22639
 MID 993531
 KEYWORDS EST.
 SOURCE This cDNA clone J05G017 library is a lambda-PRI2 strain-var Columbia vector-lambda Zip-Lox primer T7 dye primer SalI-EcoRI SalI-EcoRI-Met lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark (rootless); 4) some plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA.

ORGANISM

Arabidopsis thaliana
 Eucaryotes; Embryophyta; Magnoliophyta; Magnoliopsida; Capparidaceae; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 433)
 Newman, T., de Kraker, F., Green, F., Keegstra, K., Kendra, H., McIntosh, L., Olthrop, T., Ralston, N., Somerville, S., Thimashow, M., Reuter, E. and Somerville, C.
 Genes: a survey of a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)

TITLE

Large-scale partial sequencing of anonymous Arabidopsis cDNA clones

JOURNAL

Plant Physiol. 106, 1241-1255 (1994)

COMMENT

Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU Bldg 180, Michigan State University, Plant Biology Bldg., E. Lansing, MI
 Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 22313@clm.cmu.edu.

FEATURES

Location/Qualifiers

1..433

/organism="Arabidopsis thaliana"

/clone="J05G017"

/strain="var Columbia"

/catalytic="var Columbia"

/catalytic="var Columbia"

/catalytic="var Columbia"

/catalytic="var Columbia"

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/catalytic="var Columbia"

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18

LOCUS 722336 324 bp PCR EST 01 NOV 1996
 DEFINITION Citrus cDNA, partial sequence (pMFR1807.131).
 ACCESSION 722336
 MID 91669336
 KEYWORDS EST (expressed sequence tag).
 SOURCE Citrus unshiu (strain Miyazawa waso satsuma mandarin) at rapid developing stage (juv. sev. and pulp segment) from 10 mRNA, clone pMFR1807.131.

ORGANISM

Eucaryotes; Viridiplantae; Embryophyta; Magnoliophyta; Magnoliopsida; Rutaceae; Citrus.

REFERENCE

1 (bases 1 to 326)
 Miyazawa, T., de Kraker, F., Green, F., Keegstra, K., Kendra, H., McIntosh, L., Olthrop, T., Ralston, N., Somerville, S., Thimashow, M., Reuter, E. and Somerville, C.
 Genes: a survey of a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)

TITLE

Large-scale partial sequencing of anonymous Arabidopsis cDNA clones

JOURNAL

Plant Physiol. 106, 1241-1255 (1994)

COMMENT

Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU Bldg 180, Michigan State University, Plant Biology Bldg., E. Lansing, MI
 Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 22313@clm.cmu.edu.

FEATURES

Location/Qualifiers

1..326

/organism="Citrus unshiu"

/strain="Miyazawa waso satsuma mandarin"

/clone="pMFR1807.131"

/catalytic="var Columbia"

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19

LOCUS T15239 540 bp mRNA EST 28-JUL-1995
 DEFINITION cirs834 Ricinus communis cDNA clone pcrs834 similar to plant
 mcdm14wrb-01 fatty acid desaturase homol. fr.

ACCESSION T15239

KEYWORDS 9688892

SOURCE EST

castor bean clone pcrs834 library=lambdaz2APST strainBaker 796
 vector=lambdazAP11 primer-T3 Rsite-EcoRI Rsite2-XhoI Poly(A) RNA
 was purified from developing stage III to stage V (Greenwood &
 Bewley, Can. J. Bot. 60:1751-1760, 1982) and stem plus embryo of
 immature castor fruits. cDNA was synthesized and cloned into
 lambdaBAP1 according to the instructions of the manufacturer
 (Stratagene); synthesis was primed from the poly(A) tail, and
 cloned directionality into XhoI (3') and EcoRI (5') sites. In few
 cases, sequence data indicated that this directionality was
 reversed. Partial cDNA clones predominate.

ORGANISM

Ricinus communis
 Eucalyptaceae; Euphorbiaceae; Magnoliopsida; Rosidae;
 Euphorbiales; Euphorbiaceae; Ricinus.

1 (bases 1 to 540)

REFERENCE
 van de Loo, F.J., Turner, S. and Somerville, C.

Expressed sequence tags from developing castor seeds
 Plant Physiol. 108, 1141-1150 (1995)

COMMENT

Contact: Somerville CR
 Carnegie Institution
 290 Panama St., Stanford, CA 94305
 Tel: 415/3251521
 Email: cirs@andrew.stanford.edu
 Location/Qualifiers

FEATURES

Source

1..540
 /organism="Ricinus communis"

/clone="pcrs834"

/strain="Baker 296"

BASE COUNT 132 a 104 c 134 g 146 t 24 others

ORIGIN

Query Match

11.3%; Score 131; DB 55; Length 540;

Best Local Similarity 71.6%; Fred. No. 1,946 212;

Matches 232; Conservative 0; Mismatches 90; Indels 2; Gaps 2;

DB 79 tctatgggggcatgtgtatgttcaactttccttgcatacacaatttggag 138

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

UY 764 tctatgggggcatgtgtatgttcaactttccttgcatacacaatttggag 573

DB 139 aacatcaaacagctatccacgtatggtcatcaggaatggattggctcggggagaaa 198

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

UY 824 acnagcattcttccttccttccatcattatgcttcacatggattgcttcacacacatt 883

DB 199 tgggactgtcgatagagatlatggggttggtgaataagattatccatgaattgggaga 758

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

UY 884 tccatcaaacagctatccacgtatggtcatcaggaatggattggctcggggagaaa 943

DB 259 ctcatatggtcactcactccttgcatacgtacacattaccatgaatggaggagcacta 318

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UY 944 cctatccttgcactcactccttgcatacgtacacattaccatgaatggaggagcacta 1003

DB 319 aagcaatcaagcactaatgggtgaggtattcaggtatggtgaggtgaggtgaggtgaggt 377

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UY 1004 aagcattcaaacctcatttgcacatgattatgattatgattatgattatgattatgatt 1063

DB 378 catgtgtgagggag-caaaggagt 400

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UY 1064 ccatgttcagggagggag-caaaggagt 1087

Dec 17 17:37

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20

Search completed at Dec 17 17:37:37 1997
 Job time : 725 secs.

Dec 17 14:58

home/fallen/dec97/US-08-572-027A-1.rst2

7

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Db 16 tacttgcttggaactataggctgtaagatggtgtcctaactggtaactgggtc 75
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QY 247 TATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 106
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 atagcaacgaatggagggatcaggaatcaggaatcaggaatcaggaatcaggaat 135
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 367 ATATGCAAGCAATGCAAGCAATGCAAGCAATGCAAGCAATGCAAGCAATGCAAG 366
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 136 ggttttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 195
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 367 GATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 426
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 196 cgttcaacttcaacttcaacttcaacttcaacttcaacttcaacttcaacttca 255
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 427 AGGCAAGCAATGCAAGCAATGCAAGCAATGCAAGCAATGCAAGCAATGCAAG 486
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 tcagcaatcaatggtgtaaggaatacctcaacacacacacacacacacacacac 315
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 487 TTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 546
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 315 accttccagtttcttcttcttcttcttcttcttcttcttcttcttcttctt 375
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 547 AGGCAAGCAATGCAAGCAATGCAAGCAATGCAAGCAATGCAAGCAATGCAAG 605
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 316 gtttgaagg 384
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 606 TTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 614
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
ID AT093 standard; RNA; EST; 386 BP.
AC T040933
N1 g315253
DT 30-MAR-1993 (rel. 36, Created)
DT 12-MAR-1997 (rel. 51, last updated, Version 15)
DE 43 Arabidopsis thaliana cDNA clone c071077.
KW EST.
OS Arabidopsis thaliana (thale cress)
NC Eukaryote; mitochondrial eukaryote; Viridiplantae;
OC Charophyta; Embryophyta group; Embryophyta; Magnoliophyta;
OC Magnoliopsida; Capriferales; Brassicales; Arabidopsi.
PN 11
RP 1-386
RX MEDLINE; 90148729.
RA Newman T., deBorja F.J., Green P., Kesteven K., Kende H.,
RA McIntosh L., Oltrop J., Patrick N., Somerville C., Thomas M.,
RA Rezel E., Somerville C.
RT *Genes galore: a summary of methods for accessing results from
RT large-scale partial sequencing of anonymous Arabidopsis cDNA
RT clones*.
PL Plant Physiol. 1994;110:1107-1110.
DB AGIS; T040933; AGIS July 1995.
CC Contact: Thomas Newman MGH DOE Plant Research Laboratory, Plant
CC State University MGH DOE PRL, Michigan State University, Plant
CC Biology Bldg., E Lansing, MI 48824-1312 Fax: 517-487-4148
CC Email: t233@plant.msu.edu, tnm1312@msu.edu
FH Key Location/Qualifiers
FT source 1-386
FT /feature="Arabidopsis thaliana"
FT /clone="c071077"
FT /strain="var columbia"
FT /note="thale cress"

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Dec 17 14:58

home/fallen/dec97/US-08-572-027A-1.rst2

8

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SQ Sequence 386 bp; 84 A; 114 C; 78 G; 110 T; 0 other;
Query Match 70.8% Score 210, CR 7%, Length 386;
best local similarity 81.3% find no overlap;
Matches 315; conservative 0; Mismatches 61; Indels 4; Gaps 3;

Db 1 ctatattcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 370 CTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 429
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 cagcatcagcatcagcatcagcatcagcatcagcatcagcatcagcatcagcatc 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 430 CAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCAT 489
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ccaatcaatggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 490 CAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCAT 549
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ctcaatcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 740
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 590 CTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 609
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 gctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 296
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 610 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 669
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Db 297 ctcaatcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 356
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QY 670 CTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 729
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Db 357 ggtctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 386
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QY 730 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 789
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RESULT 6
ID AT093 standard; RNA; EST; 428 BP.
AC T228527
N1 g327668
DT 30-JUN-1994 (rel. 40, Created)
DT 15-MAR-1997 (rel. 51, last updated, Version 15)
DE 460 Arabidopsis thaliana cDNA clone T071517.
KW EST.
OS Arabidopsis thaliana (thale cress)
NC Eukaryote; mitochondrial eukaryote; Viridiplantae;
OC Charophyta; Embryophyta group; Embryophyta; Magnoliophyta;
OC Magnoliopsida; Capriferales; Brassicales; Arabidopsi.
PN 11
RP 1-428
RX MEDLINE; 90148729.
RA Newman T., deBorja F.J., Green P., Kesteven K., Kende H.,
RA McIntosh L., Oltrop J., Patrick N., Somerville C., Thomas M.,
RA Rezel E., Somerville C.
RT *Genes galore: a summary of methods for accessing results from
RT large-scale partial sequencing of anonymous Arabidopsis cDNA
RT clones*.
PL Plant Physiol. 1994;110:1107-1110.
DB AGIS; T228527; AGIS July 1995.
CC Contact: Thomas Newman MGH DOE Plant Research Laboratory, Michigan
CC State University MGH DOE PRL, Michigan State University, Plant
CC Biology Bldg., E Lansing, MI 48824-1312 Fax: 517-487-4148
CC Email: t233@plant.msu.edu, tnm1312@msu.edu
FH Key Location/Qualifiers
FT source 1-428
FT /feature="Arabidopsis thaliana"
FT /clone="T071517"
FT /strain="var columbia"
FT /note="thale cress"

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[illegible]

RESULT	8	standard; PNA; EST; 364 bp.
ID	ATT007	
AC	T46100;	
NI	9934337	
DT	10-FEB-1995 (rel. 42, created)	
DE	12-MAR-1997 (rel. 51, last updated, Version 16)	
DE	9363 Arabidopsis thaliana cDNA clone T46100.	
KW	EST	
OS	Arabidopsis thaliana (thale cress)	
OC	Eukaryotae; mitochondrial eukaryotes; Viridiplantae;	
OC	Charophyta; Embryophyta group; Embryophyta; Magnoliopsida;	
OC	Magnoliopsida; Vaparieae; Brassicaceae; Arabidopsis.	
RN	[1]	
RP	1-364	
RA	MELTING; 9514879.	
RA	Newman T., deBruijn F.J., Green P., Knevels R., Kunk H.,	
RA	McIntosh L., Ohlbrock J., Pothel N., Somerville C., Thomas M.,	
RA	Rezel E., Somerville C.,	
RT	*Genes galore: a summary of methods for accessing results from	
RT	large-scale partial sequencing of anonymous Arabidopsis cDNA	
RT	clones*;	
RT	plant Physiol. 106:1241-1256 (1994).	
DR	AS13; T46100; Accs. only 1997.	
CC	Contact: Thomas Newman MSU-East Plant Research Laboratory Michigan	
CC	State University MSU-East-PLB, Michigan State University Plant	
CC	Biology Bldg., E. Lansing MI 48824 Fax: 517-487-0864 Fax: 517-487-0168	
CC	E-mail: 2231@cnhlbm.climax.edu, NEHL gtl 924337	
EH	Key	
EH	Location/Qualifications	
FT	source	
FT	1..364	
FT	/organism="Arabidopsis thaliana"	
FT	/clone="T46100"	
FT	/strain="var Columbia"	
FT	/note="thale cress"	
FT	Sequence 364 bp; K1 A; K9 C; /u C; u; T; ik other;	

	Query Match	Similarity	16.2%	Score 167;	E= 75e-16	length 364;
	Best Local Similarity	K= 0.9	S= 0.84	Mismatch 45;	Indels 0;	Gaps 0;
	Matches	224;	Conservative	Q	Misaligned	45;
Dc	13	ggaggatctagacgcgtctggttgctttaccgcttargtgtgtgaagaagtgcgc	72			
Dc	691	GTTCAGTATCTGCGCCCTCAACAACTCCTTTCTAAGCACTGGTAAGAAGAAC	750			
Dc	73	tccatgatcttcacctcaaggagtaacggtctataafnaactnnttctgttagatc	132			
Gy	751	TGATATATTCTTATCTTATCATCTCTGCTCTCTCTCTCTCTCTCTCTCTCT	810			
Dc	133	acttaacttgcagcacactcatccctcgcttgactcaactacagattccagagtgag	192			
Gy	811	ACTTACTTCAACAACAACGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	870			
Dc	193	ctccagggggtcttggttgcacgttagaacagagatcaaggaaacttgcacaagttgcc	252			
Gy	871	TTTCAGTATCTGCGCCCTCAACAACTCCTTTCTAAGCACTGGTAAGAAGAAC	930			
Dc	253	aagatattatcaggatcactaatctgggtctatctg	281			

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Dec 17 14:58 /home/fuller/dec9/LUS-08-572-027A-1.rst2
QY      931 AATTATACCAAGGACAGACTGGTATTATA 959
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ID	RESULT	9
AC	ATT14176	standard; RNA; EST; 310 BP.
AC	T14176;	
NI	9931129	
DT	03-MAR-1997 (sep. 38)	Created
DT	12-MAR-1997 (sep. 51)	Last updated; Version 1.1
DE	4241 Arabidopsis thaliana cDNA clone 48F127.	
EW	EST.	
CC	Arabidopsis thaliana (thale cress)	
CC	Fukuyama et al. mitochondrial cytochrome c; Viridiplantae;	
CC	Chlorophyta/Eukaryophyta group; Embryophyta; Magnoliophyta;	
CC	Magnoliopsida; Euphorbiales; Brassicaceae; Arabidopsis.	
RN	11)	
RP	1-310	
RX	MEF14176; 48145729.	
RA	Newman T., deStijn F.J., Green P., Keesstra K., Kende H.,	
RA	McIntosh D., Ohlrogge J., Raithel N., Somerville S., Thomas M.,	
PA	Raizel F., Somerville C.;	
RT	*Genes: a brief summary of methods for accessing results from	
RT	large-scale partial sequencing of anonymous Arabidopsis cDNA	
RT	clones;	
RI	Plant Physiol. 106:1241-1255(1994).	
DN	AG15; 114176; AG15 July 1995.	
CC	Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan	
CC	State University MSU-DOP-PRI, Michigan State University Plant	
CC	Biotechnology Facility Lansing MI 48911-5034 Fax: 517-453-9168	
EW	Email: 2281@msu.edu; tnewman@MSU.GU 48129	
EH	Key	location/qualifiers
EH	source	1-310
FT	organism	"Arabidopsis thaliana"
FT	/clone	"48F127"
FT	/strain	"var columbica"
FT	/note	"thale cress"
CC	Sequence	310 BP; 73 A; 85 C; 65 G; 83 T; 4 other;

[illegible]

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NI 9126960
DT 19-APR-1996 (Rel. 47, Created)
DT 12-MAR-1997 (Rel. 51, Last updated, Version 4)
DE 21887 Arabidopsis thaliana cDNA clone G78377.
KM EST.
OS Arabidopsis thaliana (thale cress)
OC Eukaryotae; mitochondria; eukaryotes; Viridiplantae;
OC Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
OC Magnoliopsida; Caprales; Brassicaceae; Arabidopsis.
RN [1]
RP 1-433
RX MEDLINE; 9148729.
RA Newman T, deBruijn F.J., Green P, Kneegstra R, Kende H,
RA McIntosh L, Chibigo J, Farkas R, Somerville C, Thomas M,
RA Reisel E, Somerville C.
*Genes selected: a summary of methods for accessing results from
RT large-scale partial sequencing of anonymous Arabidopsis cDNA
RT clones?
RL Plant Physiol. 106:1241-1250 (1994).
CC Contact: Thomas Newman MSU DOE Plant Research Laboratory, Plant
CC State University MSU DOE Bldg., Michigan State University, Plant
CC Biology Bldg., E. Lansing, MI, Tel. 517-353-0854 Fax: 517-353-9168
CC Email: 223131@emc.cim.msu.edu, NCBI g1: 1269060
FH Key Location/Qualifiers
FH source 1..433
FH /organism "Arabidopsis thaliana"
FH /clone="G78377"
FH /strain="var. columbia"
FH /note="thale cress"
FT mRNA
FT Sequence 432 bp; 119 A, 106 C, 75 G, 122 T, 16 other;
SQ
Query Match 13.3% Score 153; 108 76; Length 432;
Best local similarity 79.0%, 108 A, 106 C, 75 G, 122 T, 16 other;
Matches 2287 Conservative 0% Mismatches 14; Indels 4; Gaps 6;
Db 144 tcaaacattatgttgcacagtgacacacctctctgtacacctcctgtgcgtgtctac 203
Cp 1155 ttatataattatgtttatataaataaataatgtttttatattacttgcgtgttata 1096
Db 294 atagatgaactcctttgcctcctatctacatgcgtacacacacgtgtgttcacac 263
Cp 1095 atataataacaccttctctctctctctctctctctctctctctctctctctct 1036
Db 264 gtaatggttcacacacacacacacacacacacacacacacacacacacacacac 923
Cp 1036 atataatgtttatataaataaataatgtttttatattacttgcgtgttata 977
Db 324 ggcattgtgcgagacacacacacacacacacacacacacacacacacacacac 383
Cp 976 gcaacacacacacacacacacacacacacacacacacacacacacacacacac 920
Db 384 ttgataangtccgcatatcttcttcttcttcttcttcttcttcttcttcttct 431
Cp 919 t-cttcaaatctt-gtaacttcttcttcttcttcttcttcttcttcttctt 874

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RESULT 11

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ID AT6393 standard; RNA; EST; 433 BP.
AC 126394
NI 993531
DT 21-MAR-1994 (Rel. 49, Created)
DT 12-MAR-1997 (Rel. 51, Last updated, Version 15)

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DE 4647 Arabidopsis thaliana cDNA clone 1053077.
KM EST.
OS Arabidopsis thaliana (thale cress)
OC Eukaryotae; mitochondria; eukaryotes; Viridiplantae;
OC Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
OC Magnoliopsida; Caprales; Brassicaceae; Arabidopsis.
RN [1]
RP 1-433
RX MEDLINE; 9148729.
RA Newman T, deBruijn F.J., Green P, Kneegstra R, Kende H,
RA McIntosh L, Chibigo J, Farkas R, Somerville C, Thomas M,
RA Reisel E, Somerville C.
*Genes selected: a summary of methods for accessing results from
RT large-scale partial sequencing of anonymous Arabidopsis cDNA
RT clones?
RL Plant Physiol. 106:1241-1250 (1994).
CC Contact: Thomas Newman MSU DOE Plant Research Laboratory Michigan
CC State University MSU DOE Bldg., Michigan State University, Plant
CC Biology Bldg., E. Lansing, MI, Tel. 517-353-0854 Fax: 517-353-9168
CC Email: 223131@emc.cim.msu.edu, NCBI g1: 925531
FH Key Location/Qualifiers
FH source 1..433
FH /organism "Arabidopsis thaliana"
FH /clone="1053077"
FH /strain="var. columbia"
FH /note="thale cress"
FT mRNA
FT Sequence 433 bp; 102 A, 106 C, 92 G, 113 T, 20 other;
SQ
Query Match 13.3% Score 153; 108 76; Length 433;
Best local similarity 79.0%, 108 A, 106 C, 75 G, 122 T, 16 other;
Matches 2287 Conservative 0% Mismatches 14; Indels 4; Gaps 6;
Db 197 acacacacacacacacacacacacacacacacacacacacacacacacacacacac 256
Cp 61 atataatgtttatataaataaataatgtttttatattacttgcgtgttata 120
Db 257 ggcattgtgcgagacacacacacacacacacacacacacacacacacacacac 316
Cp 121 ggcattgtgcgagacacacacacacacacacacacacacacacacacacacac 180
Db 317 atataatgtttatataaataaataatgtttttatattacttgcgtgttata 372
Cp 181 atataatgtttatataaataaataatgtttttatattacttgcgtgttata 234

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RESULT 12

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ID AT13687 standard; RNA; EST; 366 BP.
AC T13877
NI 993094
DT 07-MAR-1994 (Rel. 36, Created)
DT 12-MAR-1997 (Rel. 51, Last updated, Version 15)
DE 2052 Arabidopsis thaliana cDNA clone 43A517.
KM EST.
OS Arabidopsis thaliana (thale cress)
OC Eukaryotae; mitochondria; eukaryotes; Viridiplantae;
OC Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
OC Magnoliopsida; Caprales; Brassicaceae; Arabidopsis.
RN [1]

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[illegible][illegible]

[illegible][illegible]

[illegible]

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RESULT      3
ID           standard; RNA; EST; 509 BP.
AC          AT2456
AD          T45245f
AI          N1
AJ          4933654
DT          06-FEB-1995 (Rel. 4Z, Created)
DT          12-MAR-1997 (Rel. 5L, Last updated, Version 16)
DE          8508 Arabidopsis thaliana cDNA clone K88117.
KW          EST.
OS          Arabidopsis thaliana (thale cress)
OC          Eukaryotae; mitochondrion eukaryotes; Viridiplantae;
OC          Charophyta/Embryophyta; Embryophyta; Malvaceae;
OC          Magnoliopsida; Capriferales; Brassicaceae; Arabidopsis.
RN          N1
RP          1-509
RX          MEDLINE; 95148729.
RA          Newman T., deBourgh F.J., Green P., Proctor B., Watson R.,
RA          Mithouse L., Ollivierre S., Rankin W., Somerville C., Thomas M.,
RA          Retzel E., Somerville C.
RT          Genes galore: a summary of methods for accessing results from
RT          large-scale partial sequencing of cDNAs from Arabidopsis cDNA
RT          clones*.
RL          Plant Physiol. 106:1241-1255(1994).
DR          AGIS; T45245f; AGIS July 1995.
CC          Contact: Thomas Newman MRC Port Folio Dept of Laboratory Medicine
CC          Stree University MCC-D&E Bldg, Michigan State University, East
CC          Lansing Mich., Lansing MI tel: 517 353 0854 Fax: 517 353 9168
CC          Email: 2231stcm@dm.climson.edu URL: gis: 955654
FH          key
FH          Location/Qualifiers
FT          source
FT          1..509
FT          /organism "Arabidopsis thaliana"
FT          /color "yellow"
FT          /strain "var columbia"
FT          /note "male cross"
FT          Legend: 509 bp; and A: 49 of 50 of 147 G & others
Query Match      22.6%; Score 471; LR 149; Length 509;
Best Local Similarity 80.6%; Prod. No. 0.00e+00;
Matches 359; Conservative 0; Mismatches 82; Indels 3; Gaps 3
Db             130 atcgaagctgtgcggcgaggaaacatttttcgttgtagatctgaagaagcaatc 184
              1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Gy            1 AAGCGTGTAAAGTGSAANAATTAATAATGGTTCTCTCAAAAAATTCAAAATCAAAAT 60
              1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db             61 ATCAGAGGCGCTATCTCTGAAGAACAAGAGGCTAT ACTGTCAGAAATTAATTAATAT 120

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[illegible]

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RESULT 4
12 Accession: 574474, 0YA, EST, 386 bp
AC F049a3;
NI 9315253
ET 30-AUG-1993 (rel. 36, Created)
DT 12-MAR-1997 (rel. 51, Last updated, SeqInfo 15)
FM 4 X Arabidopsis thaliana GDA clone GEP10776,
EM EST.
OS Arabidopsis thaliana (thale cress)
OC Eukaryota; Eukaryotae; Eukaryota;
OC Eukaryota; Eukaryotae; Eukaryota;
OC Magnoliopsida; Capparidales; Brassicaceae; Arabidopsis.
[1]
RP 1-386
MIMM00F, 9514070.
BX Brown T., Jang J., P. T. Green P., Kengra K., Konde H.,
BA Katschek L., Chicago J., Ralston N., Greenville S., Thomsen M.,
BA Ralston E., Greenville C.;
ET "Genes galore: a summary of methods for accessing results from
RT large scale partial sequencing of anonymous Arabidopsis cDNA
BT clones";
PL Plant Physiol. 106:1241-1255(1994).
PE Accession: F049a3; F049a3 July 1995.
CC Contact: Thomas Newman MIM-DOE Plant Research Laboratory Michigan
CC State University MSU-DOE PRL, Michigan State University Plant
CC Biology Bldg. 61 Lansing, MI 48924-3137 Tel: 517-353-9168
CC Email: 2012@msu.edu; tnewm@doe.msu.edu, WGBI 911 314252
FH Key
FH Location/Qualifiers
FH 1-386
FH source
FH /organism="Arabidopsis thaliana"
FH /mimc="GEP10776"
FH /strain="Var columbiana"
FH /note="thale cress"
SU Sequence 386 bp; 84 A; 114 C; 78 G; 110 T; 0 other;
Query Match: 21.5%; Score 248; EB 75; Length 386;
Fast Local Similarity 84.4%; Find Pos 0.00000;

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NI 9156960
 DT 19-APR-1996 (Rel. 47, Created)
 DT 12-MAR-1997 (Rel. 51, last updated, Version 9)
 DE 21887 Arabidopsis thaliana cDNA clone G78377.
 KM EST.
 OS Arabidopsis thaliana (thale cress)
 OC Eukaryote; mitochondrial eukaryotes; Viridiplantae;
 OC Charophyta/Embryophyta group/ Embryophyta/ Magnoliophyta/
 OC Magnoliopsida/ Caprales/ Brassicaceae/ Arabidopsis.
 RN 11
 RP 1-432
 RA MEDLINE; 95148729.
 RA Newman T., deGrujic F.J., Green P., Kneegstra R., Knorr H.,
 RA McIntosh L., Olligrogge J., Ralke N., Somerville S., Thomasow M.,
 RA Rezel E., Somerville C.
 RT *Genes galore: a summary of methods for accessing results from
 RT large-scale partial sequencing of anonymous Arabidopsis cDNA
 RT clones*.
 RL Plant Physiol. 106:1241-1255 (1994).
 CC Contact: Thomas Newman MSU-P06 Plant Research Laboratory Michigan
 CC State University MSU P06 PRL, Michigan State University, Plant
 CC Biology Bldg., Lansing, MI 48911-517-353-0854 Fax: 517-353-9168
 CC Email: 2231@cam.ac.uk, clmsu.edu, MSU g1: 169060
 FH Key Location/Qualifiers
 FT source 1..432
 FT /organism="Arabidopsis thaliana"
 FT /clone="G78377"
 FT /strain="var columbia"
 FT /note="thale cress"
 FT name 1..432
 FT Sequence 432 BP, 100% A, 100% C, 100% G, 100% T, 16 other
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 Best Local Similarity 78.1% Freq. No. 9,230,243;
 Matches 225, conservative 0, Mismatches 57, Indels 6, Gaps 6,
 Db 144 tcaaaactatgtgacagatgacaaactctgtgacactccctgacggttacc 203
 Cp 1155 tcaaaactatgtgacagatgacaaactctgtgacactccctgacggttacc 1096
 Db 204 atagatgaactctgtgacactctgacatgacatgacaaaggtgtgacatgac 263
 Cp 1095 atagatgaactctgtgacactctgacatgacatgacaaaggtgtgacatgac 1036
 Db 264 gtaatgacatgacatgacatgacatgacatgacatgacatgacatgacatgac 323
 Cp 1035 atagatgaactctgtgacactctgacatgacatgacatgacatgacatgac 977
 Db 324 gtaatgacatgacatgacatgacatgacatgacatgacatgacatgacatgac 383
 Cp 977 gtaatgacatgacatgacatgacatgacatgacatgacatgacatgacatgac 430
 Db 384 ttgtaaaagtcctgctgctgctgctgctgctgctgctgctgctgctgctgct 431
 Cp 430 ttgtaaaagtcctgctgctgctgctgctgctgctgctgctgctgctgctgct 874
 RESULT 11
 ID AT6393 standard; RNA; EST; 433 BP.
 AC T22639
 NI 993531
 DT 27-JUN-1994 (Rel. 40, Created)
 DT 12-MAR-1997 (Rel. 51, last updated, Version 15)

DE 4667 Arabidopsis thaliana cDNA clone 1056107.
 KM EST.
 OS Arabidopsis thaliana (thale cress)
 OC Eukaryote; mitochondrial eukaryotes; Viridiplantae;
 OC Charophyta/Embryophyta group/ Embryophyta/ Magnoliophyta/
 OC Magnoliopsida/ Caprales/ Brassicaceae/ Arabidopsis.
 RN 11
 RP 1-433
 RA MEDLINE; 95148729.
 RA Newman T., deGrujic F.J., Green P., Kneegstra R., Knorr H.,
 RA McIntosh L., Olligrogge J., Ralke N., Somerville S., Thomasow M.,
 RA Rezel E., Somerville C.
 RT *Genes galore: a summary of methods for accessing results from
 RT large-scale partial sequencing of anonymous Arabidopsis cDNA
 RT clones*.
 RL Plant Physiol. 106:1241-1255 (1994).
 CC Contact: Thomas Newman MSU-P06 Plant Research Laboratory Michigan
 CC State University MSU P06 PRL, Michigan State University, Plant
 CC Biology Bldg., Lansing, MI 48911-517-353-0854 Fax: 517-353-9168
 CC Email: 2231@cam.ac.uk, clmsu.edu, MSU g1: 92531
 FH Key Location/Qualifiers
 FT source 1..433
 FT /organism="Arabidopsis thaliana"
 FT /clone="1056107"
 FT /strain="var columbia"
 FT /note="thale cress"
 FT name 1..433
 FT Sequence 433 BP, 100% A, 100% C, 100% G, 100% T, 20 other
 Query Match 12.4% Score 143, DB 77, Length 433;
 Best Local Similarity 78.1% Freq. No. 9,230,243;
 Matches 191, conservative 0, Mismatches 43, Indels 7, Gaps 2,
 Db 137 ttttttttttttttttttttttttttttttttttttttttttttttttttttt 196
 Cp 1 atagatgaactctgtgacactctgacatgacatgacatgacatgacatgac 60
 Db 197 atagatgaactctgtgacactctgacatgacatgacatgacatgacatgac 256
 Cp 61 atagatgaactctgtgacactctgacatgacatgacatgacatgacatgac 120
 Db 257 atagatgaactctgtgacactctgacatgacatgacatgacatgacatgac 316
 Cp 121 atagatgaactctgtgacactctgacatgacatgacatgacatgacatgac 180
 Db 317 atagatgaactctgtgacactctgacatgacatgacatgacatgacatgac 372
 Cp 372 atagatgaactctgtgacactctgacatgacatgacatgacatgacatgac 434
 RESULT 12
 ID AT13887 standard; RNA; EST; 368 BP
 AC T13887
 NI 9930914
 DT 07-MAR-1994 (Rel. 35, Created)
 DT 12-MAR-1997 (Rel. 51, last updated, Version 15)
 DE 2052 Arabidopsis thaliana cDNA clone 43557.
 KM EST.
 OS Arabidopsis thaliana (thale cress)
 OC Eukaryote; mitochondrial eukaryotes; Viridiplantae;
 OC Charophyta/Embryophyta group/ Embryophyta/ Magnoliophyta/
 OC Magnoliopsida/ Caprales/ Brassicaceae/ Arabidopsis.
 RN 11

